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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:23:55 ; Search time 52.3019 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195

Perfect score: 208
Sequence: 1 SELVEHLGNLQANQAQDGK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	208	100.0	1356	1 US-08-810-116-8	Sequence 8, Appli
2	208	100.0	1356	1 US-07-930-548A-8	Sequence 8, Appli
3	208	100.0	1356	2 US-09-098-707A-2	Sequence 2, Appli
4	208	100.0	1356	2 US-09-483-539-2	Sequence 2, Appli
5	208	100.0	1356	2 US-09-949-016-6198	Sequence 6198, Ap
6	208	100.0	1356	2 US-10-100-405A-2	Sequence 2, Appli
7	208	100.0	1356	2 US-10-022-939-2	Sequence 2, Appli
8	208	100.0	1456	2 US-09-949-016-9853	Sequence 9853, Ap
9	205	98.6	1367	1 US-07-813-593-4	Sequence 4, Appli
10	205	98.6	1367	1 US-07-977-451-6	Sequence 6, Appli
11	205	98.6	1367	1 US-07-946-507-4	Sequence 4, Appli
12	205	98.6	1367	1 US-08-252-517-6	Sequence 6, Appli
13	205	98.6	1367	1 US-07-906-397A-6	Sequence 6, Appli
14	205	98.6	1367	1 US-08-601-891-6	Sequence 6, Appli
15	205	98.6	1367	1 US-08-443-861-2	Sequence 2, Appli
16	205	98.6	1367	1 US-09-021-324-6	Sequence 6, Appli
17	205	98.6	1367	2 US-08-193-829B-2	Sequence 2, Appli
18	205	98.6	1367	2 US-09-872-136B-6	Sequence 6, Appli
19	205	98.6	1367	2 US-09-766-678-2	Sequence 2, Appli
20	205	98.6	1367	2 US-09-919-408A-6	Sequence 6, Appli
21	205	98.6	1367	4 PCT-US92-02750-8	Sequence 8, Appli
22	205	98.6	1367	4 PCT-US92-05401-6	Sequence 6, Appli
23	205	98.6	1367	4 PCT-US92-09893-6	Sequence 6, Appli
24	101	48.6	1311	1 US-08-340-011-5	Sequence 5, Appli
25	101	48.6	1311	1 US-08-901-710-5	Sequence 5, Appli
26	101	48.6	1311	2 US-09-169-079-5	Sequence 5, Appli
27	101	48.6	1338	2 US-08-750-141A-3	Sequence 3, Appli

28	101	48.6	1338	2 US-09-119-014D-6	Sequence 6, Appli
29	89	42.8	317	2 US-09-390-326-5	Sequence 5, Appli
30	89	42.8	317	2 US-09-939-833-5	Sequence 5, Appli
31	89	42.8	317	2 US-09-506-906-5	Sequence 5, Appli
32	89	42.8	317	2 US-09-939-832-5	Sequence 5, Appli
33	89	42.8	317	2 US-09-939-754-5	Sequence 5, Appli
34	89	42.8	367	2 US-09-390-326-12	Sequence 12, Appli
35	89	42.8	367	2 US-09-939-833-12	Sequence 12, Appli
36	89	42.8	367	2 US-09-506-906-12	Sequence 12, Appli
37	89	42.8	367	2 US-09-939-832-12	Sequence 12, Appli
38	89	42.8	367	2 US-09-939-754-12	Sequence 12, Appli
39	78	37.5	294	1 US-08-701-191A-17	Sequence 17, Appli
40	78	37.5	294	2 US-09-664-526-17	Sequence 17, Appli
41	68	32.7	367	2 US-09-390-326-9	Sequence 9, Appli
42	68	32.7	367	2 US-09-939-833-9	Sequence 9, Appli
43	68	32.7	367	2 US-09-506-906-9	Sequence 9, Appli
44	68	32.7	367	2 US-09-939-832-9	Sequence 9, Appli
45	68	32.7	367	2 US-09-939-754-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-810-116-8
; Sequence 8, Application US/08810116
; Patent No. 5766860
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5766860el Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,116
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/930,548
; FILING DATE: 23-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,298-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-116-8

Query Match 100.0%; Score 208; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 42
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Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 5
US-09-949-016-6198
; Sequence 6198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6198
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6198

Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 6
US-10-100-405A-2
; Sequence 2, Application US/10100405A
; Patent No. 6841367
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDC
; CURRENT APPLICATION NUMBER: US/10/100,405A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/022,939
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-100-405A-2

Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 7
US-10-022-939-2
; Sequence 2, Application US/10022939
; Patent No. 6841382
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-022-939-2

Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 8
US-09-949-016-9853
; Sequence 9853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9853
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9853

Query Match 100.0%; Score 208; DB 2; Length 1456;
Best Local Similarity 100.0%; Pred. No. 3.3e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1152 SELVEHLGNLLQANAQQDGKDYIVLPMSETLSMEEDSGLSLP 1193

;; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
;; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
;; STREET: 180 VARICK STREET
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: U.S.A.
;; ZIP: 10014
;; COMPUTER READABLE FORM: Floppy disk
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/946,507
;; FILING DATE: 19920917
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/813,593
;; FILING DATE: 24-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/793,065
;; FILING DATE: 15-NOV-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/728,913
;; FILING DATE: 28-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/679,666
;; FILING DATE: 02-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Feit, Irving N.
;; REGISTRATION NUMBER: 28,601
;; REFERENCE/DOCKET NUMBER: LEM-3-PPP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-645-1405
;; TELEFAX: 212-645-2054
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1367 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-946-507-4

Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 8.4e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLQANAQDGKDYIVLPMSSETLSMEEDSGLSLP 1193

RESULT 12
US-08-252-517-6
; Sequence 6, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/252,517
;; FILING DATE: 31-OCT-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,451
;; FILING DATE: 19-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/906,397
;; FILING DATE: 26-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US PCT/US92/05401
;; FILING DATE: 26-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: TW 81102961
;; FILING DATE: 15-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US PCT/US92/02750
;; FILING DATE: 02-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/813,593
;; FILING DATE: 24-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/793,065
;; FILING DATE: 15-NOV-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/728,913
;; FILING DATE: 28-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/679,666
;; FILING DATE: 02-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Feit, Irving N.
;; REGISTRATION NUMBER: 28,601
;; REFERENCE/DOCKET NUMBER: LEM-3-7P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-645-1405
;; TELEFAX: 212-645-2054
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1367 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-252-517-6

Query Match 98.6%; Score 205; DB 1; Length 1367;
Best Local Similarity 97.6%; Pred. No. 8.4e-21;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLQANAQDGKDYIVLPMSSETLSMEEDSGLSLP 1193

RESULT 13
US-07-906-397A-6
; Sequence 6, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.

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; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/906,397A
; APPLICATION NUMBER: US/07/906,397A
; FILING DATE: 19920626
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-906-397A-6
;
; Query Match 98.6%; Score 205; DB 1; Length 1367;
; Best Local Similarity 97.6%; Pred. No. 8.4e-21;
; Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMERDGLSLP 42
; Db 1152 SELVEHLGNLQANAQQDGKDYIVLPMSSETLSMEEDSGLSLP 1193
;
; RESULT 14
; US-08-601-891-6
; Sequence 6, Application US/08601891
; Patent No. 5747651
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,891
; FILING DATE: 15-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451
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; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-601-891-6
;
; Query Match 98.6%; Score 205; DB 1; Length 1367;
; Best Local Similarity 97.6%; Pred. No. 8.4e-21;
; Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
; Db 1152 SELVEHLGNLQANAQQDGKDYIVLPMSSETLSMEEDSGLSLP 1193
;
; RESULT 15
; US-08-443-861-2
; Sequence 2, Application US/08443861
; Patent No. 5851999
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Risau, Werner
; APPLICANT: Millauer, Birgit
; APPLICANT: Gazit, Aviv
; APPLICANT: Levitzki, Alex
; TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
; TITLE OF INVENTION: Endothelial Growth Factor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,861

FILING DATE: 22-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/193,829

FILING DATE: 09-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-060

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212)869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1367 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-443-861-2

Query Match 98.6%; Score 205; DB 1; Length 1367;

Best Local Similarity 97.6%; Pred. No. 8.4e-21;

Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

Search completed: December 9, 2005, 10:35:49

Job time : 53.3019 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:20:05 ; Search time 232.189 Seconds
(without alignments)
127.621 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195

Perfect score: 208

Sequence: 1 SELVEHLGNLQNAQQDK.....IVLPISLTSMEDSGLSLP 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208	100.0	180	2	Q8M123 ovine aries
2	208	100.0	207	2	Q9N112 SHEEP
3	208	100.0	1356	1	VGFR2 HUMAN
4	208	100.0	1451	2	Q59BB0 HUMAN
5	205	98.6	341	2	Q8CD05 MOUSE
6	205	98.6	1343	1	VGFR2 RAT
7	205	98.6	1343	2	Q5PQU0 RAT
8	205	98.6	1345	2	Q8VCD0 MOUSE
9	205	98.6	1367	1	VGFR2 MOUSE
10	193	92.8	178	2	Q9X554 RABIT
11	183	88.0	1348	1	VGFR2 COTJA
12	183	88.0	1348	2	Q677M1 CHICK
13	145	69.7	346	2	Q42570 XENLA
14	114.5	55.0	464	2	Q5RIP2 BRARE
15	114.5	55.0	829	2	Q5T334 BRARE
16	114.5	55.0	1357	2	Q5GIT4 BRARE
17	113	54.3	1328	2	Q4RWK3 TETNG
18	108	51.9	367	2	Q91356 COTCO
19	108	51.9	1379	2	P79701 COTCO
20	103	49.5	1336	1	VGFR1 RAT
21	102	49.0	136	2	Q9MZE3 MACMU
22	102	49.0	1333	1	VGFR1 MOUSE
23	101	48.6	453	2	Q9CW58 MOUSE
24	101	48.6	551	2	Q59G09 HUMAN
25	101	48.6	1338	2	VGFR1 HUMAN
26	101	48.6	1338	2	Q5TAR1 HUMAN
27	100	48.1	62	2	Q6Q2B9 FIG
28	100	48.1	116	2	Q9NOK8 FIG
29	99	47.6	86	2	Q8SPL3 HORSE
30	99	47.6	87	2	Q8WMP2 HORSE
31	99	47.6	107	2	Q9GJZ8_CALJA

32	97	46.6	107	2	Q8MIM8 CAPHI	Q8mim8 capra hircu
33	97	46.6	153	2	Q28210 BOVIN	Q28210 bos taurus
34	97	46.6	221	2	Q9N111 SHEEP	Q9n111 ovine aries
35	91.5	44.0	1327	2	Q8OHL3 CHICK	Q8ghl3 gallus gall
36	89	42.8	487	2	Q75WK4 ORYLA	Q75wk4 oryzias lat
37	89	42.8	1302	1	VGFR2 ERARE	Q8axb3 brachydanio
38	84	40.4	1331	2	Q4SS72 TETNG	Q4ss72 tetraodon n
39	82	39.4	1387	2	Q4SJQ3 TETNG	Q4sfjq3 tetraodon n
40	77	37.0	1272	2	Q4JDD5 BRARE	Q4jdd5 brachydanio
41	77	37.0	1272	2	Q5GIT3 BRARE	Q5git3 brachydanio
42	64	30.8	4488	2	Q9QZHI MOUSE	Q9qzh1 mus musculus
43	62	29.8	323	2	Q92WY1 RHIME	Q92wy1 rhizobium m
44	62	29.8	5162	2	Q70LM6 BREBE	Q70lm6 brevivacill
45	61.5	29.6	402	2	Q4K3F2 PSEF5	Q4k3f2 pseudomonas

ALIGNMENTS

RESULT 1
Q8M123 SHEEP
ID Q8M123_SHEEP PRELIMINARY; PRT; 180 AA.
AC Q8M123;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vascular endothelial growth factor receptor-2 (Fragment).
OS Ovis aries (Sheep). Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placental artery endothelium;
RA Chung J.-Y., Tsou S.C.M., Wen Y.-X., Magness R.R., Zheng J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF534634; AAN04105.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8M123; 1-150.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 180
SQ SEQUENCE 180 AA; 20599 MW; 70B5F444574779A0 CRC64;

Query Match 100.0%; Score 208; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQNAQQDKYIVLPISLTSMEDSGLSLP 42
|||
DB 136 SELVEHLGNLQNAQQDKYIVLPISLTSMEDSGLSLP 177
|||

RESULT 2

Q9N112 SHEEP
ID Q9N112_SHEEP PRELIMINARY; PRT; 207 AA.
AC Q9N112;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

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DE KDR/flk-1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Scholz T.D., Segar J.L.;
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF233076; AAF60280.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q9N112; 1-157.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS01834; VEGFR2.
DR PROSITE; PS00001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1
FT NON_TER 207
FT NON_TER 207
SQ SEQUENCE 207 AA; 23691 MW; 51C3950D82F988F6 CRC64;

Query Match 100.0%; Score 208; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.5e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDKYIVLPISSETLSMEEDSGLSLP 42
DB 143 SELVEHLGNLLQANAQQDKYIVLPISSETLSMEEDSGLSLP 184

RESULT 3
VGFR2 HUMAN STANDARD; PRT; 1356 AA.
AC P35968; O60723; Q14178;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Kinase insert domain receptor) (Protein-tyrosine kinase
DE receptor Flk-1).
GN Name=KDR; Synonyms=Flk1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yin L.Y., Wu Y., Patterson C.;
RA "Full length human KDR/flk-1 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Umbilical vein;
RA Yu Y., Whitney R.G., Sato J.D.;
RT "Coding region for human VEGF receptor KDR (VEGFR-2)";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 3-1356.
RC TISSUE=Umbilical vein;
RX MEDLINE=92019839; PubMed=1656371;
RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.;
RA Shows T.B.;

```

"Identification of a new endothelial cell growth factor receptor tyrosine kinase."; Oncogene 6:1677-1683(1991).

[4]

NUCLEOTIDE SEQUENCE OF 1-22. MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111; Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E., Harber E.;

"Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).

[5]

FUNCTION.

MEDLINE=93038639; PubMed=1417831; Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D., Arallino D.C., Gospodarowicz D., Boehlen P.;

"Identification of the KDR tyrosine kinase as a receptor for vascular endothelial cell growth factor."; Biochem. Biophys. Res. Commun. 187:1579-1586(1992).

-1- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein kinase activity. The VEGF-kinase ligand/receptor signaling system plays a key role in vascular development and regulation of vascular permeability.

-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.

-1- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like) domains.

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EMBL; AF035121; AAB88005.1; -; mRNA.

EMBL; AF063658; AAC16450.1; -; mRNA.

EMBL; X61656; CAA43837.1; -; mRNA.

EMBL; L04947; AAA59459.1; -; mRNA.

EMBL; X89776; CAA61916.1; -; Genomic_DNA.

PIR; JCI402; JCI402.

PDB; 1VR2; X-ray; A=806-1171.

Ensembl; ENSG00000128052; Homo sapiens.

HGNC; HGNC:6307; KDR.

MM; 191306; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005021; F:vascular endothelial growth factor receptor. . ; TAS.

GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_c2.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR001824; Recepttyr_kinsIII.

InterPro; IPR001245; Tyr_kinase.

InterPro; IPR008266; Tyr_kinase_AS.

InterPro; IPR009134; VEGFR.

InterPro; IPR009136; VEGFR2.

PRINTS; PR01832; VEGFRECEPTOR.

PRINTS; PR01834; VEGFRECEPTR2.

ProDom; PD000001; Prot_kinase; 2.

SMART; SM00408; IGC2; 2.

SMART; SM00219; Tyrkc; 1.

PROSITE; PS0835; IG_LIKE; 5.

PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

3D-structure; Angiogenesis; ATP-binding; Developmental protein; Differentiation; Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.

SIGNAL 1 19 Potential.

FT	CHAIN	20	1356	Vascular endothelial growth factor receptor 2.
FT	TOPO_DOM	20	764	Extracellular (Potential).
FT	TRANSMEM	765	789	Potential.
FT	TOPO_DOM	790	1356	Cytoplasmic (Potential).
FT	DOMAIN	46	110	Ig-like C2-type 1.
FT	DOMAIN	141	207	Ig-like C2-type 2.
FT	DOMAIN	224	320	Ig-like C2-type 3.
FT	DOMAIN	328	414	Ig-like C2-type 4.
FT	DOMAIN	421	548	Ig-like C2-type 5.
FT	DOMAIN	551	660	Ig-like C2-type 6.
FT	DOMAIN	667	753	Ig-like C2-type 7.
FT	DOMAIN	834	1162	Protein kinase.
FT	NP_BIND	840	848	ATP (By similarity).
FT	ACT_SITE	1028	1028	By similarity.
FT	BINDING	868	868	ATP (By similarity).
FT	MOD_RES	1059	1059	phosphotyrosine (by autocatalysis) (By similarity).
FT	CARBOHYD	46	46	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	66	66	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	96	96	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	143	143	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	158	158	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	245	245	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	318	318	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	374	374	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	395	395	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	511	511	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	523	523	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	580	580	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	613	613	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	619	619	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	631	631	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	675	675	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	704	704	N-linked GlcNAc. .) (Potential).
FT	CARBOHYD	721	721	N-linked GlcNAc. .) (Potential).
FT	VARIANT	297	297	V -> I (in dbSNP:2305948).
FT	VARIANT	472	472	/FTId=VAR_022071.
FT	VARIANT	472	472	Q -> H (in dbSNP:1870377).
FT	CONFLICT	2	2	/FTId=VAR_020353.
FT	CONFLICT	772	772	Q -> E (in Ref. 2).
FT	CONFLICT	787	787	A -> T (in Ref. 3).
FT	CONFLICT	835	835	R -> G (in Ref. 3).
FT	CONFLICT	848	848	K -> N (in Ref. 3).
FT	CONFLICT	1347	1347	V -> E (in Ref. 3).
FT	SEQUENCE	1356 AA;	151527 MW;	S -> T (in Ref. 3).
SQ	SEQUENCE	1356 AA;	59E7C4B05CFEBB3 CRC64;	
	Query Match	100.0%;	Score 208;	DB 1;
	Best Local Similarity	100.0%;	Length 1356;	
	Matches	Conservative	0;	Mismatches
			0;	Indels
				Gaps
Oy	1 SELVEHLGNLQAQQDGKDYIVLPISETLSMEEDSGLSLP 42			
Db	1154 SELVEHLGNLQAQQDGKDYIVLPISETLSMEEDSGLSLP 1195			
RESULT 4				
Q59EB0_HUMAN				
ID Q59EB0_HUMAN PRELIMINARY;				PRT; 1451 AA.
AC Q59EB0;				
DT 10-MAY-2005 (TrEMBLrel. 30, Created)				
DD 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)				
DE Kinase insert domain receptor (A type III receptor tyrosine kinase variant [fragment].				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;				
OC Homo.				
OX NCBI_TaxID=9606;				
RP NUCLEOTIDE SEQUENCE.				
[1]				

```

RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tonaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the ENBL/GenBank/DBJ databases.
DR EMBL; AK031739; BAC27532.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8CD05; 1-162.
DR MGI; MGI:96683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR GO; GO:0030097; P:hemoiesis; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Kinase; Receptor.
FT NON_TER
SQ
SEQUENCE 341 AA; 38302 MW; EB4DCC4BB481195 CRC64;
Query Match 98.6%; Score 205; DB 2; Length 341;
Best Local Similarity 97.6%; Pred. No. 3.3e-18;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQANQAGKQYIVLPISSETLSMEEDSGLSLP 42
DB 148 SELVEHLGNLQANQAGKQYIVLPISSETLSMEEDSGLSLP 189
RESULT 6
VEGFR2_RAT
ID AC O08775; STANDARD; PRT; 1343 AA.
DT 16-OCT-2001 (Rel. 40, Last Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1).
GN Name=Kdr; Synonyms=Flk1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. CSP-1/PDGF
CC receptor subfamily.
CC -1- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U93306; AB97508.1; -; mRNA.
DR EMBL; U93307; AB97509.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR RGD; 2965; Kdr.
DR GO; GO:0019838; F:growth factor binding; IMP.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IMP.
DR GO; GO:0048010; P:vascular endothelial growth factor receptor. .; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinasIII.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyRkc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR Angiogenesis; ATP-binding; Developmental protein; Differentiation;
DR Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
DR Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1343 Vascular endothelial growth factor
FT receptor 2.
FT TOPO_DOM 20 760 Extracellular (Potential).
FT TRANSMEM 761 782 Potential.
FT TOPO_DOM 783 1343 Cytoplasmic (Potential).

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FT DOMAIN 46 109 IG-like C2-type 1.
FT DOMAIN 141 207 IG-like C2-type 2.
FT DOMAIN 224 320 IG-like C2-type 3.
FT DOMAIN 328 414 IG-like C2-type 4.
FT DOMAIN 421 540 IG-like C2-type 5.
FT DOMAIN 547 654 IG-like C2-type 6.
FT DOMAIN 663 749 IG-like C2-type 7.
FT DOMAIN 830 1158 Protein kinase.
FT NP_BIND 836 844 ATP (By similarity).
FT ACT_SITE 1024 1024 By similarity.
FT BINDING 864 864 ATP (By similarity).
FT MOD_RES 1055 1055 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 96 96 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 318 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 395 395 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 576 576 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 609 609 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 615 615 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 627 627 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 671 671 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 700 700 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 717 717 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1343 AA; 150394 MW; AD7E509EB62D3FF4 CRC64;

Query Match 98.6%; Score 205; DB 1; Length 1343;
Best Local Similarity 97.6%; Pred. No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKYIVLPISETLSMEEDSGLSLP 42
DB 1150 SELVEHLGNLQANAQQDGKYIVLPMSSETLSMEEDSGLSLP 1191

RESULT 7
Q5PQU0 RAT PRELIMINARY; PRT; 1343 AA.
AC Q5PQU0_2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Kdr protein.
GN Name=Kdr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hulton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Director MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087029; AAH87029.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR00719; prot_kinase.
DR InterPro; IPR001824; RecepttyrkinalI.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; Igc2; 5.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ SEQUENCE 1343 AA; 150274 MW; F4B906E8012A5C59 CRC64;

Query Match 98.6%; Score 205; DB 2; Length 1343;
Best Local Similarity 97.6%; Pred. No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKYIVLPISETLSMEEDSGLSLP 42
DB 1150 SELVEHLGNLQANAQQDGKYIVLPMSSETLSMEEDSGLSLP 1191

RESULT 8
Q8VCD0 MOUSE PRELIMINARY; PRT; 1345 AA.
ID Q8VCD0_MOUSE PRELIMINARY;
AC Q8VCD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinase insert domain protein receptor.
GN Name=Kdr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020530; AAH20530.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR Ensembl; ENSMUSG0000062960; Mus musculus.
DR MGI; MGI:96683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001824; RecepttyrkinasIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1345 AA; 150460 MW; 11859F8A58A33A39 CRC64;

Query Match 98.6%; Score 205; DB 2; Length 1345;
Best Local Similarity 97.6%; Pred. No. 1.5e-17;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQQKQYIVLPISSETLSMEEDSGLSLP 42
DB 1152 SELVEHLGNLQANAQQQKQYIVLPMSSETLSMEEDSGLSLP 1193

RESULT 9
VFGR2 MOUSE
ID VFGR2 MOUSE STANDARD; PRT; 1367 AA.
AC P35918;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1) (Kinase NYK).
GN Name=Kdr; Synonyms=Flk-1, Flk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Embryo;
RX MEDLINE=93208880; PubMed=7681362; DOI=10.1016/0092-8674(93)90573-9;
RA Millauer B., Witzigmann-Voos S., Schnurch H., Martinez R.,
RA Mueller N.P.H., Risaau W., Ullrich A.;
RT "High affinity VEGF binding and developmental expression suggest Flk-1
RL as a major regulator of vasculogenesis and angiogenesis."; Cell 72:835-846(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/He; TISSUE=Fetal liver;
RX MEDLINE=92020984; PubMed=1717995;
RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,
RA Lemishcka I.R.;
RT "A receptor tyrosine kinase cDNA isolated from a population of
RT enriched primitive hematopoietic cells and exhibiting close genetic
RL linkage to c-kit."; Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93141255; PubMed=8423988;
RA Oelrichs R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.;
RT "NYK/Flk-1: a putative receptor protein tyrosine kinase isolated from
RT E10 embryonic neuroepithelium is expressed in endothelial cells of the
RL developing embryo."; Oncogene 8:11-18(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-15.
RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RL receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION.
RX MEDLINE=93361481; PubMed=8356051;
RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;
RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth
RT factor and is selectively expressed in vascular endothelium."; Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).
RL CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed at high levels in adult heart, lung,
CC kidney, brain and skeletal muscle, but is also expressed at lower
CC levels in most other adult tissues.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X70842; CAA50192.1; -; mRNA.
DR EMBL; X59397; CAA42040.1; -; mRNA.
DR EMBL; S53103; AAB25043.1; -; mRNA.
DR EMBL; X89777; CAA61917.1; -; Genomic_DNA.
DR PIR; A41228; A41228.
DR HSSP; P35968; 1VR2.
DR Ensembl; ENSMUSG00000062960; Mus musculus.

MGI; MGI:96683; Kdr.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0045165; P:cell fate commitment; IMP.
 DR GO; GO:0016477; P:cell migration; IGI.
 DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
 DR GO; GO:0030097; P:hemoopoiesis; IMP.
 DR GO; GO:0001570; P:vasculogenesis; IMP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig c2.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR01824; RecepttyrkinIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR InterPro; IPR009134; VEGFR.
 DR InterPro; IPR009136; VEGFR2.
 DR Pfam; PF00047; ig; 1.
 DR PRINTS; PR01832; VEGFRECEPTOR.
 DR PRINTS; PR01834; VEGFRECEPTR2.
 DR ProDom; PD000001; Prot_kinase; 2.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00835; IG-LIKE; 5.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 KW Angiogenesis; ATP-binding; Developmental protein; Differentiation;
 KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
 KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 1367 Vascular endothelial growth factor receptor 2.
 FT TOPO_DOM 20 762 Extracellular (Potential).
 FT TRANSMEM 763 784 Potential.
 FT TOPO_DOM 785 1367 Cytoplasmic (Potential).
 FT DOMAIN 46 111 Ig-like C2-type 1.
 FT DOMAIN 143 209 Ig-like C2-type 2.
 FT DOMAIN 226 325 Ig-like C2-type 3.
 FT DOMAIN 330 416 Ig-like C2-type 4.
 FT DOMAIN 423 542 Ig-like C2-type 5.
 FT DOMAIN 549 656 Ig-like C2-type 6.
 FT DOMAIN 665 751 Ig-like C2-type 7.
 FT DOMAIN 832 1160 Protein kinase.
 FT NP_BIND 838 846 ATP (By similarity).
 FT ACT_SITE 1026 1026 By similarity.
 FT BINDING 866 866 ATP (By similarity).
 FT MOD_RES 1057 1057 Phosphotyrosine (by autocatalysis) (By similarity).
 FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 247 247 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 320 320 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 397 397 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 521 521 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 611 611 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 617 617 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 629 629 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 673 673 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 702 702 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 719 719 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 25 25 P -> T (in Ref. 1).
 FT CONFLICT 679 679 G -> D (in Ref. 3).
 FT CONFLICT 783 784 LV -> VL (in Ref. 1).
 FT CONFLICT 917 917 S -> C (in Ref. 1).
 FT CONFLICT 1341 1367 QLTSLGSGVFPAPPPTGNHGRGA -> RSPPV (in Ref. 3).
 FT SEQUENCE 1367 AA; 152517 MW; EFC99704FIDCA266 CRC64;

Query Match 98.6%; Score 205; DB 1; Length 1367;
 Best Local Similarity 97.6%; Pred. No. 1.5e-17;
 Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 42
 DB 1152 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 1193
 RESULT 10
 Q9XS54_RABIT PRELIMINARY; PRT; 178 AA.
 AC Q9XS54;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE VEGF receptor-2/Flk-1 (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Japanese white; TISSUE=Liver;
 RA Umeki K., Kon K., Ohtaki S.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017155; BAA76520.1; -; mRNA.
 DR HSSP; P35968; IVR2.
 DR SMR; Q9XS54; 1-150.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Receptor.
 FT NON_TER 1 178
 FT NON_TER 178 178
 FT SEQUENCE 178 AA; 20363 MW; BSFID072A2D0A477 CRC64;
 Query Match 92.8%; Score 193; DB 2; Length 178;
 Best Local Similarity 92.9%; Pred. No. 5.9e-17;
 Matches 39; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 42
 DB 136 SELVEHLGNLLOANAQQGKDYIVLPISETLSMEEDSGLSLP 177
 RESULT 11
 VGFR2_COTJA STANDARD; PRT; 1348 AA.
 ID VGFR2_COTJA
 AC P52583;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
 DE (VEGFR-2) (Endothelial kinase receptor EK1) (Quek 1).
 DE Names:KDR; Synonyms=EK1, FLK-1;
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OC NCBI_TaxID=93934;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA MEDLINE=97017121; PubMed=8863722; DOI=10.1016/0378-1119(96)00159-X;
RX Eichmann A., Marcelle C., Breat C., Le Douarin N.M.;
RT "Molecular cloning of Quak 1 and 2, two quail vascular endothelial
RL growth factor (VEGF) receptor-like molecules."; Gene 174:3-8(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 910-1348.
RC TISSUE=Spinal cord;
RX MEDLINE=93378866; PubMed=8396413; DOI=10.1016/0925-4773(93)90096-G;
RA Eichmann A., Marcelle C., Breat C., Le Douarin N.M.;
RT "Two molecules related to the VEGF receptor are expressed in early
RL endothelial cells during avian embryonic development."; Mech. Dev. 42:33-48(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 764-880, AND CHARACTERIZATION.
RC TISSUE=Embryo;
RX MEDLINE=95301109; PubMed=7781909; DOI=10.1006/dbio.1995.1180;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1)
RL are expressed during vasculogenesis and vascular differentiation in
RN the quail embryo."; Dev. Biol. 169:699-712(1995).
RP NUCLEOTIDE SEQUENCE OF 1023-1079.
RC PubMed=1281306;
RA Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RL the avian embryo."; Oncogene 7:2479-2487(1992).
CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In all endothelial tissues during onset of
CC vascularization. In later development, present in lung, heart,
CC intestine and skin.
CC -!- DEVELOPMENTAL STAGE: Expressed in whole mesoderm at onset of
CC gastrulation. From day 2, confined to endothelial tissues and
CC expression continues to be widespread throughout vascularization
CC until E9 where it becomes restricted to specific regions such as
CC the spinal chord and heart valves.
CC -!- INDUCTION: In vitro, it is induced by basic fibroblast growth
CC factor (bFGF), uniquely in the first 24 hours of cell culture.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X83288; CAA58268.1; -; mRNA.
CC EMBL; S65205; AAB28127.1; -; mRNA.
CC EMBL; S78345; AAB34594.1; -; mRNA.
CC PIR; JC4953; S51656.
CC HSP; P35968; 1VR2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig C2.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR01824; RecepttyrkinIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR008266; Tyr_pkinase_AS.
CC InterPro; IPR009134; VEGFR.
CC InterPro; IPR009136; VEGFR2.
CC Pfam; PF00047; ig; 1.

DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR PRODOM; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Phosphoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 1348 Vascular endothelial growth factor
FT receptor 2.
FT TOPO_DOM 21 756 Extracellular (Potential).
FT TRANSMEM 757 777 Potential.
FT TOPO_DOM 778 1348 Cytoplasmic (Potential).
FT DOMAIN 43 106 Ig-like C2-type 1.
FT DOMAIN 138 202 Ig-like C2-type 2.
FT DOMAIN 220 312 Ig-like C2-type 3.
FT DOMAIN 320 405 Ig-like C2-type 4.
FT DOMAIN 412 534 Ig-like C2-type 5.
FT DOMAIN 540 651 Ig-like C2-type 6.
FT DOMAIN 658 744 Ig-like C2-type 7.
FT DOMAIN 825 1155 Protein kinase.
FT NP_BIND 831 839 ATP (By similarity).
FT ACT_SITE 1021 1021 By similarity.
FT BINDING 859 859 ATP (By similarity).
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 63 63 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 153 153 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 240 240 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 365 365 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 386 386 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 556 556 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 603 603 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 613 613 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 666 666 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 688 688 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 710 710 N-linked (GlcNAc...) (Potential).
FT CONFLICT 865 865 A -> S (in Ref. 3).
SQ SEQUENCE 1348 AA; 150306 MW; A5B4194A76FD5FB3 CRC64;
Query Match 88.0%; Score 183; DB 1; Length 1348;
Best Local Similarity 83.3%; Pred. No. 1.2e-14;
Matches 35; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 SELVEHLGNLIQANAOQDKDYIVLPISETLSMEEDSGLSLP 42
DB 1147 SELVEHLGNLIQANVROQDKDYVVLPLSVLSINMEEDSGLSLP 1188
RESULT 12
Q677M1_CHICK
ID Q677M1_CHICK PRELIMINARY; PRT; 1348 AA.
AC Q677M1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE Vascular endothelial growth factor receptor 2.
GN Name=Flkl;
OS Gallus gallus (Chicken).

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauroida; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hashimoto T.;
RT "Modulation of retinal neurogenesis by vascular endothelial growth
factor.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY382882; AAR26285.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PRO1832; VEGFRECEPTOR.
DR PRINTS; PRO1834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG_7.
DR SMART; SM00408; IGc2; 5.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00835; IG_LIKE_5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Receptor.
SQ SEQUENCE 1348 AA; 150121 MW; F6EF0F21CA839D5E CRC64;

Query Match 88.0%; Score 183; DB 2; Length 1348;
Best Local Similarity 83.3%; Pred. No. 1.2e-14;
Matches 35; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1147 SELVEHLGNLQANVRQDGKDYIVLPISVLSNIEDSGVSLP 1198

RESULT 13
O42570 XENLA PRELIMINARY; PRT; 346 AA.
AC O42570;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Receptor tyrosine kinase (Fragment).
GN Names=flk-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Head;
```

```
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RT "Neovascularization of the Xenopus embryo.";
RL Dev. Dyn. 0:0-0(1997).
DR EMBL; AF007760; AAB63281.1; -; mRNA.
DR HSP; P35968; 1VR2.
DR SMR; O42570; 1-164.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PRO0109; TYRKINASE.
DR PRINTS; PRO1834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Kinase; Receptor.
FT NON_TER 1 346
FT NON_TER 346 346
SQ SEQUENCE 346 AA; 38976 MW; AA35FA8F0C702416 CRC64;

Query Match 69.7%; Score 145; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 2.5e-10;
Matches 28; Conservative 10; Mismatches 2; Indels 2; Gaps 1;

OY 1 SELVEHLGNLQANQAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 150 SELVEHLGNLQASAHQDGKDYI--PLTVSLNIEDSGVSM 189

RESULT 14
Q5RIP2 BRARE PRELIMINARY; PRT; 464 AA.
AC Q5RIP2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein similar to vertebrate kinase insert domain receptor (A
DE type III receptor tyrosine kinase) (KDR) (Fragment).
GN Name=OTTDARP0000004701; ORFNames=BUSM1-205D10.1-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248242; CA11526.1; -; Genomic DNA.
DR Ensembl; ENSDARG00000017321; Danio rerio.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR001245; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor; Transferase.
FT NON_TER 1 464
FT NON_TER 464 464
SQ SEQUENCE 464 AA; 52430 MW; FA84BBA573F7DC88 CRC64;

Query Match 55.0%; Score 114.5; DB 2; Length 464;
Best Local Similarity 69.4%; Pred. No. 3.5e-06;
Matches 25; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SELVEHLGNLLQANAQDGKDYIVLPISFETLSMEED 36
Db 400 TQLVEHLGNLLQASAQDGKDYIPLTNGE---MEEE 432

RESULT 15
Q5TZ34_BRARE
ID Q5TZ34_BRARE PRELIMINARY; PRT; 829 AA.
AC Q5TZ34;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel kinase insert domain receptor protein (Fragment).
GN Name=OTTDARP0000004831; ORFNames=CH211-254J6.1-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OK NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX511058; CAH68950.1; -; Genomic DNA.
DR Ensembl; ENSDARG00000017321; Danio rerio.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR002290; Ser thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50035; IG LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Receptor; Transferase; Transmembrane.
FT NON_TER 1 829
FT NON_TER 829 829
SQ SEQUENCE 829 AA; 92982 MW; 6PFAE9BD19856F51 CRC64;

Query Match 55.0%; Score 114.5; DB 2; Length 829;
Best Local Similarity 69.4%; Pred. No. 6.7e-06;
Matches 25; Conservative 4; Mismatches 4; Indels 3; Gaps 1;
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Qy 1 SELVEHLGNLLQANAQDGKDYIVLPISFETLSMEED 36
Db 645 TQLVEHLGNLLQASAQDGKDYIPLTNGE---MEEE 677
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Search completed: December 9, 2005, 10:33:47
Job time : 234.189 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:21:00 ; Search time 36.4528 Seconds
(without alignments)
110.858 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195

Perfect score: 208

Sequence: 1 SELVEHLGNLLQANAQQDGK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	1356	JC1402	protein-tyrosine k
2	205	98.6	1367	A41228	protein-tyrosine k
3	183	88.0	1348	S51656	vascular endotheli
4	108	51.9	367	B56598	endothelial kinase
5	108	51.9	1379	JC4954	vascular endotheli
6	103	49.5	1330	S49010	embryonic receptor
7	103	49.5	1336	I60598	Fit-1 tyrosine kin
8	102	49.0	1333	I78875	receptor tyrosine
9	101	48.6	1338	S09982	protein-tyrosine k
10	62	29.8	323	E95864	probable ABC trans
11	60	28.8	334	F71480	probable flagellar
12	60	28.8	450	S42825	serum response fac
13	59.5	28.6	1288	A48999	protein-tyrosine k
14	59	28.4	186	D83083	probable two-compo
15	59	28.4	595	JC6550	sex-determining re
16	57.5	27.6	175	C70453	translation initia
17	57.5	27.6	903	F82080	preprotein translo
18	57.5	27.6	1018	T30853	antigenic heat-sta
19	56.5	27.2	859	T35785	probable beta-gluc
20	55	26.4	286	T21545	hypothetical prote
21	55	26.4	323	AH3187	nitrotriacetate
22	55	26.4	372	T28027	hypothetical prote
23	55	26.4	1663	C3HU	complement C3 prec
24	54.5	26.2	1058	T19282	hypothetical prote
25	54	26.0	109	AD1600	B. subtilis YnaA p
26	54	26.0	160	B89841	hypothetical prote
27	54	26.0	906	AD3267	protein translocas
28	54	26.0	1118	1SYBVC	carbamoyl-phosphat
29	53.5	25.7	470	S71466	homeotic protein S

30	53.5	25.7	627	2	B83692	hypothetical prote
31	53.5	25.7	799	2	T00052	hypothetical prote
32	52.5	25.2	619	2	F82387	hypothetical prote
33	52.5	25.2	1026	2	C97783	cell surface antig
34	52.5	25.2	1363	2	I58375	protein-tyrosine k
35	52.5	25.2	1630	2	T40217	hypothetical prote
36	52	25.0	332	2	F81743	conserved hypotet
37	52	25.0	340	2	A10195	DNA-directed DNA p
38	52	25.0	534	2	B96642	hypothetical prote
39	52	25.0	623	2	T16384	hypothetical prote
40	52	25.0	1026	2	T05882	hypothetical prote
41	51.5	24.8	413	2	E70177	acetate kinase (ac
42	51.5	24.8	612	2	E84809	hypothetical prote
43	51.5	24.8	864	2	S60441	hypothetical prote
44	51.5	24.8	1066	2	S50237	TATA box-binding p
45	51.5	24.8	2004	2	T30185	hypothetical prote

ALIGNMENTS

RESULT 1

JC1402 protein-tyrosine kinase (EC 2.7.1.112) KDR - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 05-Oct-2004
C:Accession: JC1402; I58357
R:Terman, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Gosp
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
A:Title: Identification of the KDR tyrosine kinase as a receptor for vascular endothelial
A:Reference number: JC1402; MUID:93038639; PMID:1417831
A:Accession: JC1402
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-616, 'E', 618-700, 'E', 702-748, 'F', 750-1263, 'I', 1265-1290, 'P', 1292
A:Cross-references: UNIPROT:F35988; UNIPARC:UPI000017A3C3; EMBL:X61656; NID:931717
R:Terman, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.; Shows, T.B.
Oncogene 6, 1677-1683, 1991
A:Title: Identification of a new endothelial cell growth factor receptor tyrosine kinase
A:Reference number: I58357; MUID:92019839; PMID:1656371
A:Accession: I58357
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 3-1356 <TER2>
A:Cross-references: UNIPARC:UPI000016A991; GB:I04947; NID:G186674; PIDN:AAA59459.1; PID
C:Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.

Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

A41228 protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept
C:Species: Mus musculus (house mouse)
C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004
R:Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.
C:Accession: A41228; A46085; I58365; S18832; S29991
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A:Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primiti

F;856-1188/Domain: protein kinase homology <KIN>
F;864-872/Region: protein kinase ATP-binding motif

Query Match 51.9%; Score 108; DB 2; Length 1379;
Best Local Similarity 54.8%; Pred. No. 1.7e-05;
Matches 23: Conservative 8; Mismatches 9; Indels 2; Gaps 1;

QY 1 SELVEHLGNLLQANAQQDGKQYIVLPISETILSMEEDSGLSLP 42
| : | | | | | | | | | | | | | : | : | : | : | : |
Db 1175 SDLVEILGNLLQENVQOEGKOYI--PLNDHSHSEDDGFSQVP 1214

RESULT 6

S49010
embryonic receptor kinase - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C/Accession: S49010
R/Choi, K.; Wall, C.; Hanratty, R.; Keller, G.
Oncogene 9, 1261-1266, 1994
A/Title: Isolation of a gene encoding a novel receptor tyrosine kinase from differentiat
A/Reference number: S49010; MUID:94181281; PMID:8134130
A/Accession: S49010
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1330 <CHO>
A/Cross-references: UNIPROT:P35969; UNIPARC:UIPT000016CD30; EMBL:X78568; NID:g510664; PID:
C/Keywords: ATP
F/823-1158/Domain: protein kinase homology <KIN>
F/831-839/Region: protein kinase ATP-binding motif

Query Match 49.5%; Score 103; DB 2; Length 1330;
Best Local Similarity 54.8%; Pred. No. 7.2e-05;
Matches 23: Conservative 6; Mismatches 11; Indels

```

QY      1 SELVEHILNLLQANAQQDGKDYIVLPISETLSMEEDSGISLP 42
          :|||||:|||||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|
Dp     1145 AELVEKIGDLLOANVOODGKDYI--PLNAILTRNSNFYSTP 1184

```

RESULT 7

160598
 Fit-1 tyrosine kinase receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
 C:Accession: I60598
 R:Yamane, A.; Seetharam, L.; Yamaguchi, S.; Gotoh, N.; Takahashi, T.; Neufeld, G.; Shibui
 Oncogene 9, 2683-2690, 1994
 A:Title: A new communication system between hepatocytes and sinusoidal endothelial cells
 A:Reference number: I60598; MUID:94336223; PMID:8058332
 A:Accession: I60598
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1336 <RES>
 A:Cross-references: UNIPROT:P53767; UNIPARC:UPI0000138774; GB:D28498; NID:G511662; PIDN:
 C:Keywords: ATP
 F:825-1161/Domain: protein kinase homology <XIN>
 F:833-841/Region: protein kinase ATP-binding motif

Query Match 49.5%; Score 103; DB 2; Length 1336;
Best Local Similarity 54.8%; Pred. No. 7.2e-05;
Matches 23; Conservative 6; Mismatches 11; Indels

```

QY      1 SELVEHLGNLLQANAQQDGKDYIVLPISSETLSMEEDSGLSLP 42
      :||| |||:||||| ||| ||| |||: |||: |||
Dh     1148 AELVEKIGNLIQANVOOGKDYI--PINALITRNSGETYSVP 1182

```

RECITE O

receptor tyrosine kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence revision
02-Aug-1996 #text change 05-Oct-2004
RESULT 8
I78875

C;Accession: I78875
C;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Morberg, D.M.; Kriz, R.; Morris, J
Oncogene 8, 2293-2298, 1993
A;Title: Molecular cloning of murine FLT and FLT4.
A;Reference number: I58375; MUID:93330572; PMID:8393164
A;Accession: I78875
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1333 <RES>
A;Cross-references: UNIPROT:P35969; UNIPARC:UPI0000028DE1; GB:L07297; NID:G293782; PIDN
C;Genetics:
A;Gene: FLT
C;Keywords: ATP
F:826-1161/Domain: protein kinase homology <KIN>
F:834-842/Region: protein kinase ATP-binding motif

Query Match 49.0%; Score 102; DB 2; Length 1333;
Best Local Similarity 54.8%; Pred. No. 9.7e-05;
Matches 23; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
:
: : : : : : : : : : : :
: : : : : : : : : : : :
: : : : : : : : : : : :
: : : : : : : : : : : :

DH 1148 AELVEKIGDNLQANVOODGKYI--PINAILTRNSSFYSTP 1187

SECRET

RESULT 9
 S09982
 protein-tyrosine kinase (EC 2.7.1.112) fltl precursor - human
 N:Alternate names: receptor-type tyrosine kinase flt
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Oct-2004
 C:Accession: S09982
 R:Shibuya, M.; Yanaguchi, S.; Yamane, A.; Ikeda, T.; Tojo, A.; Matsushime, H.; Sato, M.
 Oncogene 5, 519-524, 1990
 A:Title: Nucleotide sequence and expression of a novel human receptor-type tyrosine kin
 A:Reference number: S09982; MUID:90221591; PMID:2158038
 A:Accession: S09982
 A:Molecule type: mRNA
 A:Residues: 1-1338 <SHR>
 A:Cross-references: UNIPROT:P17948; UNIPARC:UPI0000138773; EMBL:X51602; NID:g31431; PID:
 C:Genetics:

; Gene: [G08T1332](#); Map position: [13q12-13q12](#); Keywords: ATP, autophosphorylation; glycoprotein; membrane protein; phosphoprotein; Cross-references: [GDB:120616](#); [OMIM:165070](#)

Query Match 48.6%; Score 101; DB 2; Length 1338;
Best Local Similarity 57.1%; Pred. No. 0.00013;
Matches 24: Conservative 4; Mismatches 12; Indels 2; Gaps 1;

```
QY      1 SELVEHLNLLQAANAQQDGKDYIVLPISETILSMEEDSGLSLP 42
        :|||||:||||| |||||| |::: |: |
db     1148 AEIVEKI GDLI AANVOODGKYI --PINALTGNGSTFYSTP 1187
```

DEC 11 1964

A:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: E95864
 R:Finan, T.W.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan-
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo-
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: E95864
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-323 <KUR>

A;Cross-references: UNIPROT:Q92WY1; UNIPARC:UPI00000CB441; GB:AL591985; PIDN:CAC48581.1									
A;Experimental source: strain 1021, megaplasmid pSymb									
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, J. P.; Chai, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.									
Science 293, 668-672, 2001									
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, J.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.									
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.									
A;Reference number: A96039; MUID:21368234; PMID:11474104									
A;Contents: annotation									
C;Genetics:									
A;Gene: SMB20181									
A;Genome: plasmid									
Query Match 29.8%; Score 62; DB 2; Length 323;									
Best Local Similarity 41.2%; Pred. No. 2.8;									
Matches 14; Conservative 8; Mismatches 8; Indels 4; Gaps 2;									
Qy	13 ANAQODGKDYIVLPISST---LSWEEDSGL-SLP 42								
Db	89 ANQRASGKDYFIPYRAVGGLMKVDDSGIKALP 122								
RESULT 11									
F71480									
probable flagellar m-ring protein - Chlamydia trachomatis (serotype D, strain UW3/Cx)									
C;Species: Chlamydia trachomatis									
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004									
C;Accession: F71480									
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, S.									
Science 282, 754-759, 1998									
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis									
A;Reference number: A71570; MUID:99000809; PMID:9784136									
A;Accession: F71480									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-334 <ARN>									
A;Cross-references: UNIPROT:O84724; UNIPARC:UPI00000D338F; GB:AE001342; GB:AE001273; NID									
A;Experimental source: serotype D, strain UW-3/Cx									
C;Genetics:									
A;Gene: flfF									
Query Match 28.8%; Score 60; DB 2; Length 334;									
Best Local Similarity 41.5%; Pred. No. 5.2;									
Matches 22; Conservative 4; Mismatches 13; Indels 14; Gaps 3;									
Qy	4 VEHLGNL----LQANQAQDGKDYI----VLPISETLSMEEDS-----GLSLP 42								
Db	57 LSHLGNLQSIQAKKEQLEKDLTFEPVLQATVLSQEEEDSLAEISVILSLP 109								
RESULT 12									
S42825									
serum response factor homolog - fruit fly (Drosophila melanogaster)									
C;Species: Drosophila melanogaster									
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004									
C;Accession: S42825									
R;Groppe, J.C.									
submitted to the EMBL Data Library, February 1994									
A;Reference number: S42825									
A;Accession: S42825									
A;Status: preliminary									
A;Molecule type: mRNA									
A;Residues: 1-450 <GRO>									
A;Cross-references: UNIPROT:Q24535; UNIPARC:UPI0000135F3A; EMBL:X77532; NID:G453586; PID									
C;Genetics:									
A;Gene: FlyBase:Serf									
A;Cross-references: FlyBase:FBgn0010354									
F;166-221/Domain: serum response factor DNA-binding domain homology <SRF>									
Query Match 28.8%; Score 60; DB 2; Length 450;									
Best Local Similarity 45.0%; Pred. No. 7.3;									

Matches	9;	Conservative	6;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	11 LQANAQQGKDYIVLPISET 30								
Db	390 LQVHAEDGNGYVITPLSST 409								
RESULT 13									
A48999									
protein-tyrosine kinase (EC 2.7.1.112) flt4 precursor - human									
N;Alternate names: class III receptor tyrosine kinase FLT4; fms-like tyrosine kinase 4									
C;Species: Homo sapiens (man)									
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004									
C;Accession: A48999; A44930; G02316; S36130; A42010									
R;Pajusola, K.; Aprelikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara, L.; Alitalo, R.									
Cancer Res. 52, 5738-5743, 1992									
A;Title: FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops and is e									
A;Reference number: A48999; MUID:93007958; PMID:1327515									
A;Accession: A48999									
A;Status: preliminary; not compared with conceptual translation									
A;Molecule type: mRNA									
A;Residues: 1-1298 <PAJ>									
A;Cross-references: UNIPROT:P35916; UNIPARC:UPI0000138777; PIDN:AAB23636.1; PID:G257352									
A;Experimental source: HEL erythroleukemia cells									
A;Note: sequence extracted from NCBI backbone (NCBIP:115335)									
R;Aprelikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Alitalo, R.; Bailey, S.K.;									
Cancer Res. 52, 746-748, 1992									
A;Title: FLT4, a novel Class III receptor tyrosine kinase in chromosome 5q33-qter.									
A;Reference number: A44930; MUID:92119639; PMID:1310071									
A;Accession: A44930									
A;Status: preliminary; not compared with conceptual translation									
A;Molecule type: mRNA									
A;Residues: 761-1190 <APR>									
A;Cross-references: UNIPARC:UPI000017A3EA; GB:X68203; NID:G31433									
A;Note: sequence extracted from NCBI backbone (NCBIP:78155)									
R;Wood, W.I.									
submitted to the EMBL Data Library, December 1995									
A;Reference number: H01039									
A;Accession: G02316									
A;Status: translated from GB/EMBL/DBJ									
A;Molecule type: mRNA									
A;Residues: 1-1298 <WOO>									
A;Cross-references: UNIPARC:UPI0000138777; EMBL:U43143; NID:g1150990; PIDN:AAA85215.1; P									
R;Galland, F.									
submitted to the EMBL Data Library, December 1992									
A;Reference number: S36130									
A;Accession: S36130									
A;Molecule type: mRNA									
A;Residues: 1-23, 'D', 25-744, 'P', 746-751, 'RP', 754-889, 'Q', 891-1127, 'V', 1129-1145, 'H', 1147									
A;Cross-references: UNIPARC:UPI00003CA99; EMBL:X69878; NID:G297049; PIDN:CAA49505.1; PI									
R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.									
Genomics 13, 475-478, 1992									
A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.									
A;Reference number: A42010; MUID:92307693; PMID:1319394									
A;Accession: A42010									
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra									
A;Molecule type: mRNA									
A;Residues: 776-889, 'Q', 891-1127, 'V', 1129-1145, 'H', 1147-1163, 'D', 1165-1200 <GAL2>									
A;Cross-references: UNIPARC:UPI000017A3EB									
C;Genetics:									
A;Gene: GDB:FLT4									
A;Cross-references: GDB:128732; OMIM:136352									
A;Map position: 5q34-5q35									
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane									
F;1-23/Domain: signal sequence #status predicted <SIG>									
F;24-1298/Product: protein-tyrosine kinase FLT4 #status predicted <MAT>									
F;843-1176/Domain: protein kinase homology <KIN>									
F;851-859/Region: protein kinase ATP-binding motif									
Query Match 28.6%; Score 59.5; DB 2; Length 1298;									
Best Local Similarity 45.9%; Pred. No. 28;									
Matches 17; Conservative 6; Mismatches 13; Indels 1; Gaps 1;									

QY 1 SELVHGLNLQNAQQDGKDYIVLPISFTLSMEEDS 37
 ||||| ||||| : : : : :
 Db 1163 SELVEILGDLQGRGLQEEVEVCMAPRS-SQSSEGS 1198

RESULT 14

D83083
 probable two-component response regulator PA4493 [imported] - Pseudomonas aeruginosa (sp
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Jun-2003
 C:Accession: D83083
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: D83083
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-186 <STO>
 A:Cross-references: UNIPARC:UPI00000C5D35; GB:AE004863; GB:AE004091; NID:G9950731; PIDN:
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4493
 C:Superfamily: response regulator, RegA/PrrA/ActR type; response regulator homology

Query Match 28.4%; Score 59; DB 2; Length 186;
 Best Local Similarity 58.6%; Pred. No. 3.6;
 Matches 17; Conservative 0; Mismatches 8; Indels 4; Gaps 1;

QY 13 ANAQDQGDYIVLPISFTLSMEEDSGLSL 41
 ||||| ||||| ||||| |||||
 Db 50 ALAQDTPDYAVL-----DLMEGDSGLVL 74

RESULT 15

JC6550
 sex-determining region Y gene-related protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 15-Mar-2004
 C:Accession: JC6550
 R:Kido, S.; Hiraoka, Y.; Ogawa, M.; Sakai, Y.; Yoshimura, Y.; Aiso, S.
 Gene 208, 201-206, 1998
 A:Title: Cloning and characterization of mouse mSox13 cDNA.
 A:Reference number: JC6550; MUID:98201614; PMID:9524265
 A:Accession: JC6550
 A:Molecule type: mRNA
 A:Residues: 1-595 <KID>
 A:Cross-references: UNIPARC:UPI000016C745; DDBJ:AB006329; NID:G3077735; PIDN:BAA25786.1;
 A:Experimental source: embryo
 C:Comment: This protein is capable of binding the AACAT sequence.
 C:Genetics:
 A:Gene: sox13
 C:Keywords: embryo; leucine zipper
 F:395-470/Domain: HMG box homology <HMG1>

Query Match 28.4%; Score 59; DB 2; Length 595;
 Best Local Similarity 35.7%; Pred. No. 14;
 Matches 15; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

QY 5 EHLGNLLQNAQQDGKDYIVLP-----SETLSMEEDSGLSLP 42
 : ||||| ||||| : : : : :
 Db 184 QHKINLLQQIQVNNPYNIPAPFPFSHQPLPVPDPSQLALP 225

Search completed: December 9, 2005, 10:34:39
 Job time : 38.4528 secs

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OM protein - protein search, using sw model

Run on: December 9, 2005, 11:21:30 ; Search time 63 Seconds
(without alignments)
278.553 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195
Perfect score: 208
Sequence: 1 SELVEHLGNLQNAQQDGK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208	100.0	429	US-10-664-421-44	Sequence 44, Appl
2	208	100.0	429	US-10-941-635-44	Sequence 44, Appl
3	208	100.0	567	US-10-327-414-8	Sequence 8, Appl
4	208	100.0	1306	US-10-741-600-1470	Sequence 1470, Ap
5	208	100.0	1354	US-10-262-538-30	Sequence 30, Appl
6	208	100.0	1354	US-10-669-176-30	Sequence 30, Appl
7	208	100.0	1356	US-09-969-037-7	Sequence 7, Appl
8	208	100.0	1356	US-10-022-939-2	Sequence 2, Appl
9	208	100.0	1356	US-10-100-405A-2	Sequence 2, Appl
10	208	100.0	1356	US-10-327-414-6	Sequence 6, Appl
11	208	100.0	1356	US-10-090-183-2	Sequence 2, Appl
12	208	100.0	1356	US-10-165-193A-11	Sequence 11, Appl
13	208	100.0	1356	US-10-394-322A-66	Sequence 66, Appl
14	208	100.0	1356	US-10-440-464-129	Sequence 129, App
15	208	100.0	1356	US-10-783-528-61	Sequence 61, Appl
16	208	100.0	1356	US-10-872-198-115	Sequence 115, App
17	208	100.0	1356	US-10-763-276-7	Sequence 7, Appl
18	208	100.0	1356	US-10-741-600-1469	Sequence 1469, Ap
19	208	100.0	1356	US-10-741-600-1471	Sequence 1471, Ap
20	208	100.0	1356	US-10-926-806-10	Sequence 10, Appl
21	208	100.0	1356	US-10-824-982-2	Sequence 2, Appl
22	208	100.0	1356	US-11-021-951-115	Sequence 115, App
23	205	98.6	1345	US-10-090-183-6	Sequence 6, Appl
24	205	98.6	1367	US-09-919-408-6	Sequence 6, Appl
25	205	98.6	1367	US-09-766-678-2	Sequence 2, Appl
26	205	98.6	1367	US-09-872-136-6	Sequence 6, Appl
27	205	98.6	1367	US-10-165-193A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-664-421-44
; Sequence 44, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIVAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 44
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-44

Query Match 100.0%; Score 208; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 5.1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQNAQQDGKQYIVLPISETLSMEEDSGLSLP 42
DB 371 SELVEHLGNLQNAQQDGKQYIVLPISETLSMEEDSGLSLP 412

RESULT 2

US-10-941-635-44
; Sequence 44, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15

Best Local Similarity 100.0%; Pred. No. 2.1e-19; Indels 0; Gaps 0; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1104 SELVEHLGNLLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1145

RESULT 5
US-10-262-538-30
Sequence 30, Application US/10262538
Publication No. US20030113324A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
FILE REFERENCE: 28967/37564
CURRENT APPLICATION NUMBER: US/10/262,538
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 1354
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-538-30

Query Match 100.0%; Score 208; DB 4; Length 1354;
Best Local Similarity 100.0%; Pred. No. 2.2e-19; Indels 0; Gaps 0; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 6
US-10-669-176-30
Sequence 30, Application US/10669176
Publication No. US20040214766A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: VEGF-C OR VEGF-D MATERIALS AND METHODS FOR TREATMENT OF
FILE REFERENCE: 28967/37564B
CURRENT APPLICATION NUMBER: US/10/669,176
CURRENT FILING DATE: 2003-09-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 1354
TYPE: PRT
ORGANISM: Homo sapiens
US-10-669-176-30

Query Match 100.0%; Score 208; DB 4; Length 1354;
Best Local Similarity 100.0%; Pred. No. 2.2e-19; Indels 0; Gaps 0; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 7
US-09-969-037-7
Sequence 7, Application US/09969037
Publication No. US2003002247A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
FILE REFERENCE: for 1175-tyrosine phosphorylated KDR/Fik-1 and usages of the same
CURRENT APPLICATION NUMBER: US/09/969,037

; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-09-969-037-7

Query Match 100.0%; Score 208; DB 3; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 8

US-10-022-939-2
; Sequence 2, Application US/10022939
; Publication No. US20030032160A1
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-022-939-2

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 9

US-10-100-405A-2
; Sequence 2, Application US/10100405A
; Publication No. US20030055239A1
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDC
; CURRENT APPLICATION NUMBER: US/10/100,405A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/022,939
; PRIOR FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-100-405A-2

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 10

US-10-327-414-6
; Sequence 6, Application US/10327414
; Publication No. US20030158083A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin G
; TITLE OF INVENTION: A Method of Effecting angiogenesis by Modulating the Function of
; TITLE OF INVENTION: Endothelia Phosphatase
; FILE REFERENCE: 8864M
; CURRENT APPLICATION NUMBER: US/10/327,414
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/355,125
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-414-6

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 11

US-10-090-183-2
; Sequence 2, Application US/10090183
; Publication No. US20030185802A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ralph A. Reisfeld
; APPLICANT: Andrew G. Niethammer
; APPLICANT: Rong Xiang
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-829.0
; CURRENT APPLICATION NUMBER: US/10/090,183
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT

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; ORGANISM: human
US-10-090-183-2

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 12
US-10-165-193A-11
; Sequence 11, Application US/10165193A
; Publication No. US20030207391A1
; GENERAL INFORMATION:
; APPLICANT: HELEN PAPPA
; TITLE OF INVENTION: BINDING PROTEIN
; FILE REFERENCE: 1396-1-00
; CURRENT APPLICATION NUMBER: US/10/165,193A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: PCT/GB00/04693
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: GB9928950.6
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-193A-11

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 13
US-10-394-322A-66
; Sequence 66, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-66

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 14
US-10-440-464-129
; Sequence 129, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-129

Query Match      100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 15
US-10-783-528-61
; Sequence 61, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-783-528-61

Query Match      100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 16
US-10-872-198-115
```


Sequence 115, Application US/10872198
Publication No. US20050002897A1
GENERAL INFORMATION:
APPLICANT: Ulrich HAUPTS
APPLICANT: Andre KOLTERMANN
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMEIER
APPLICANT: Ulrich Kettling
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.000204
CURRENT APPLICATION NUMBER: US/10/872,198
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
LENGTH: 1356
TYPE: PRT
ORGANISM: Homo sapiens
US-10-872-198-115

Query Match 100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||

Db 1154 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 17

US-10-763-276-7
Sequence 7, Application US/10763276
Publication No. US20050004003A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Substance which inhibits binding of information
TITLE OF INVENTION: transfer molecule for 1175-tyrosine phosphorylated KDR/Flk-1
TITLE OF INVENTION: and usages of the same
FILE REFERENCE: 249-199
CURRENT APPLICATION NUMBER: US/10/763,276
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/969,037B
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: JP 2000-303694
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/263,512
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1356
TYPE: PRT
ORGANISM: Human
US-10-763-276-7

Query Match 100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||

Db 1154 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 18
US-10-741-600-1469
Sequence 1469, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1469
LENGTH: 1356
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-600-1469

Query Match 100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||

Db 1154 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 19

US-10-741-600-1471
Sequence 1471, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1471
LENGTH: 1356
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-600-1471

Query Match 100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||

Db 1154 SELVEHLGNLQANQQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 20

US-10-926-806-10
Sequence 10, Application US/10926806
Publication No. US20050096257A1
GENERAL INFORMATION:
APPLICANT: SHIMA, DAVID
APPLICANT: CALIAS, PERRY
APPLICANT: ADAMIS, ANTHONY P.
TITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
TITLE OF INVENTION: NEOVASCULAR DISORDERS
FILE REFERENCE: 112089.184 EYE-013
CURRENT APPLICATION NUMBER: US/10/926,806
CURRENT FILING DATE: 2004-08-26
PRIOR APPLICATION NUMBER: 60/556,837

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; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 60/498,407
; PRIOR FILING DATE: 2003-08-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-806-10

Query Match          100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 21
US-10-824-982-2
; Sequence 2, Application US/10824982
; Publication No. US20050197492A1
; GENERAL INFORMATION:
; APPLICANT: Inventors: Michele A. McTigue, Steven L. Bender, Allen Borchardt, Robert
; APPLICANT: S.
; APPLICANT: Kania, Chris Pinko, John A. Wickersham
; TITLE OF INVENTION: Crystal Structure of VEGFRK2: Ligand Complexes and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: PC19173A
; CURRENT APPLICATION NUMBER: US/10/824,982
; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-824-982-2

Query Match          100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 22
US-11-021-951-115
; Sequence 115, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTIS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMIEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-115

Query Match          100.0%; Score 208; DB 6; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 23
US-10-090-183-6
; Sequence 6, Application US/10090183
; Publication No. US20030185802A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ralph A. Reisfeld
; APPLICANT: Andrew G. Niethammer
; APPLICANT: Rong Xiang
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-829.0
; CURRENT APPLICATION NUMBER: US/10/090,183
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1345
; TYPE: PRT
; ORGANISM: mouse
US-10-090-183-6

Query Match          98.6%; Score 205; DB 4; Length 1345;
Best Local Similarity 97.6%; Pred. No. 5.7e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 24
US-09-919-408-6
; Sequence 6, Application US/09919408
; Patent No. US20020072077A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/919,408
  FILING DATE: 31-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/977,451
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 07/906,397
  FILING DATE: 26-JUN-1992
  APPLICATION NUMBER: US PCT/US92/05401
  FILING DATE: 26-JUN-1992
  APPLICATION NUMBER: TW 81102961
  FILING DATE: 15-APR-1992
  APPLICATION NUMBER: US PCT/US92/02750
  FILING DATE: 02-APR-1992
  APPLICATION NUMBER: US 07/813,593
  FILING DATE: 24-DEC-1991
  APPLICATION NUMBER: US 07/793,065
  FILING DATE: 15-NOV-1991
  APPLICATION NUMBER: US 07/728,913
  FILING DATE: 28-JUN-1991
  APPLICATION NUMBER: US 07/679,666
  FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Feit, Irving N.
  REGISTRATION NUMBER: 28,601
  REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 212-645-1405
  TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1367 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-919-408-6

Query Match      98.6%; Score 205; DB 3; Length 1367;
Best Local Similarity 97.6%; Pred. No. 5.8e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 25
US-09-766-678-2
Sequence 2, Application US/09766678
Patent No. US20020081650A1
GENERAL INFORMATION:
  APPLICANT: Ullrich, Axel
             Rieau, Werner
             Millauer, Birgit
             Gazit, Aviv
             Levitzki, Alex
  TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
                    Endothelial Growth Factor
  NUMBER OF SEQUENCES: 6
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds
    STREET: 1155 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: U.S.A.
    ZIP: 10036-2711
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/766,678
  FILING DATE: 25-Jan-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/193,829
  FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Coruzzi, Laura A.
  REGISTRATION NUMBER: 30,742
  REFERENCE/DOCKET NUMBER: 7683-060
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212)790-9090
  TELEFAX: (212)869-9741
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1367 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-766-678-2

Query Match      98.6%; Score 205; DB 3; Length 1367;
Best Local Similarity 97.6%; Pred. No. 5.8e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1152 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

RESULT 26
US-09-872-136-6
Sequence 6, Application US/09872136
Patent No. US20020119545A1
GENERAL INFORMATION:
  APPLICANT: Lemischka, Ihor R.
  TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
                    RECEPTORS AND THEIR LIGANDS
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: ImClone Systems Incorporated
    STREET: 180 Varick Street
    CITY: New York
    STATE: New York
    COUNTRY: U.S.A.
    ZIP: 10014
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/872,136
    FILING DATE: 01-Jun-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/208,786
    FILING DATE: <Unknown>
    APPLICATION NUMBER: US/09/021,324
    FILING DATE: <Unknown>
    APPLICATION NUMBER: US/07/977,451
    FILING DATE: 1992-11-19
    APPLICATION NUMBER: US 07/906,397
    FILING DATE: 26-JUN-1992
    APPLICATION NUMBER: US PCT/US92/05401
    FILING DATE: 26-JUN-1992
    APPLICATION NUMBER: TW 81102961
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; FILING DATE: 15-APR-1992
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-872-136-6

Query Match          98.6%; Score 205; DB 3; Length 1367;
Best Local Similarity 97.6%; Pred. No. 5.8e-19;
Matches 41; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB      1152 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1193

Search completed: December 9, 2005, 11:25:46
Job time : 64 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2005, 10:29:01 ; Search time 9.50943 Seconds
(without alignments)
24.665 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195

Perfect score: 208
Sequence: 1 SELVEHLGNLQANQDQK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	48.6	1338	6	US-10-821-234-1622
2	101	48.6	1338	7	US-11-109-156-23
3	55	26.4	1663	6	US-10-982-545-6
4	50.5	24.3	383	6	US-10-982-545-6
5	48.5	23.3	170	7	US-10-467-657-3226
6	48	23.1	478	6	US-11-069-642-12
7	48	23.1	581	6	US-10-467-657-3994
8	48	23.1	752	6	US-10-793-626-28
9	48	23.1	1304	6	US-10-793-626-1036
10	47	22.6	530	6	US-10-821-234-1648
11	47	22.6	530	6	US-10-878-556A-71
12	46	22.1	184	6	US-10-878-556A-148
13	46	22.1	215	6	US-10-131-826A-76
14	46	22.1	358	6	US-10-467-657-2286
15	46	22.1	434	6	US-10-467-657-6970
16	46	22.1	564	6	US-10-467-657-6894
17	45	21.6	136	6	US-10-485-517-298
18	45	21.6	139	6	US-10-793-626-1970
19	45	21.6	165	6	US-10-793-626-1644
20	45	21.6	948	6	US-10-793-626-844
21	45	21.6	1071	6	US-10-485-517-131
22	45	21.6	4374	7	US-10-467-657-1654
23	44.5	21.4	205	6	US-11-128-572-2
24	44.5	21.4	215	6	US-10-793-626-2156
25	44.5	21.4	372	6	US-10-793-626-1102
					Sequence 2840, Ap

26	44.5	21.4	499	6	US-10-467-657-2096
27	44	21.2	82	6	US-10-353-783-59
28	44	21.2	208	6	US-10-353-783-46
29	44	21.2	272	7	US-11-082-389-76
30	44	21.2	273	6	US-10-353-783-48
31	44	21.2	273	6	US-10-353-783-49
32	44	21.2	273	6	US-10-353-783-61
33	44	21.2	558	6	US-10-467-657-694
34	43.5	20.9	520	6	US-10-467-657-3948
35	43	20.7	287	6	US-10-467-657-2768
36	43	20.7	304	6	US-10-467-657-7410
37	43	20.7	349	7	US-11-074-176-84
38	43	20.7	435	6	US-10-510-386-62
39	43	20.7	700	7	US-11-169-630-5
40	43	20.7	954	6	US-10-467-962B-31
41	43	20.7	1145	6	US-10-793-626-1432
42	42.5	20.4	214	6	US-10-467-657-7796
43	42.5	20.4	403	7	US-11-074-176-354
44	42.5	20.4	408	7	US-11-074-176-186
45	42.5	20.4	696	7	US-11-080-991-46

ALIGNMENTS

RESULT 1
US-10-821-234-1622
; Sequence 1622, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1622
; LENGTH: 1338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1622

Query Match 48.6%; Score 101; DB 6; Length 1338;
Best Local Similarity 57.1%; Pred. No. 5.6e-06;
Matches 24; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
QY 1 SELVEHLGNLQANQDQKDYIVLPISETLSMEEDSGLSLP 42
Db 1148 AELVERKGLDQANQDQKDYI--PINAILTNGSGFTYSTP 1187

RESULT 2
US-11-109-156-23
; Sequence 23, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki

RESULT 7
US-10-793-626-28
; Sequence 28, Application US/10793626
; Publication No. US20050255478A1

; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt seq_genes Version 1.0
 ; SEQ ID NO 1648
 ; LENGTH: 1304
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-821-234-1648

Query Match 23.1%; Score 48; DB 6; Length 1304;
 Best Local Similarity 36.8%; Pred. No. 71;
 Matches 14; Conservative 5; Mismatches 9; Indels 10; Gaps 2;

Qy 1 SELVEHLGNLQANAQQDGKDYI--VLPISITLSMEED 36
 Db 1152 SFLEFYIGEM-----GKDYIYAVTPLEDALMDRD 1181

RESULT 10
 US-10-878-556A-71
 ; Sequence 71, Application US/10878556A
 ; Publication No. US20050266399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoffmann La-Roche Inc.
 ; TITLE OF INVENTION: HCV regulated protein expression
 ; FILE REFERENCE: 21762
 ; CURRENT APPLICATION NUMBER: US/10/878,556A
 ; CURRENT FILING DATE: 2004-06-28
 ; NUMBER OF SEQ ID NOS: 199
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 71
 ; LENGTH: 530
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: sw_hum/kpy2_human
 ; DATABASE ENTRY DATE: 1990-04-01
 US-10-878-556A-71

Query Match 22.6%; Score 47; DB 6; Length 530;
 Best Local Similarity 27.3%; Pred. No. 33;
 Matches 9; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 10 LLOANAQQDGKDYIVLPISITLSMEEDSGLSLP 42
 Db 179 LISLQVKQKGADFLVTEVNGSGSLGSKGVNLP 211

RESULT 11
 US-10-878-556A-148
 ; Sequence 148, Application US/10878556A
 ; Publication No. US20050266399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoffmann La-Roche Inc.
 ; TITLE OF INVENTION: HCV regulated protein expression
 ; FILE REFERENCE: 21762
 ; CURRENT APPLICATION NUMBER: US/10/878,556A
 ; CURRENT FILING DATE: 2004-06-28
 ; NUMBER OF SEQ ID NOS: 199
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 148
 ; LENGTH: 530
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: sw_hum/kpy1_human
 ; DATABASE ENTRY DATE: 1990-04-01
 US-10-878-556A-148

Query Match 22.6%; Score 47; DB 6; Length 530;
 Best Local Similarity 27.3%; Pred. No. 33;
 Matches 9; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 10 LLOANAQQDGKDYIVLPISITLSMEEDSGLSLP 42
 Db 179 LISLQVKQKGADFLVTEVNGSGSLGSKGVNLP 211

RESULT 12
 US-10-131-826A-76
 ; Sequence 76, Application US/10131826A
 ; Publication No. US20050245730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Berorge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C128
 ; CURRENT APPLICATION NUMBER: US/10/131,826A
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 76
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-131-826A-76

Query Match 22.1%; Score 46; DB 6; Length 184;
 Best Local Similarity 31.7%; Pred. No. 12;
 Matches 13; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

Qy 4 VEHLGNL-LOANAQQDGKDYI-VLPISITLSMEEDSGLSLP 42
 Db 96 LQHLKALDLRSNQDFPEQLTALPALETINLENEIVDVP 136

RESULT 13
 US-10-467-657-2286
 ; Sequence 2286, Application US/10467657


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; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: FONTANA Mariagrazia
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2286
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-2286

Query Match 22.1%; Score 46; DB 6; Length 2
Best Local Similarity 28.2%; Pred No. 15;
Matches 11; Conservative 9; Mismatches 19; Indels 19

QY 4 VEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
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DB 171 VQGIIGGIFQISIEGSPGIMGLPVYETVSMQLDGLGVRPP 209

RESULT 14
US-10-467-657-6970
; Sequence 6970, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6970
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6970

Query Match 22.1%; Score 46; DB 6; Length 3
Best Local Similarity 37.5%; Pred. No. 28;
Matches 12; Conservative 5; Mismatches 13; Indels 13

QY 5 EHLGNLLQANAQQDGKDYIVLPISETLSMEED 36
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DB 132 EHLKNLLKKNVGKFRDTFIV--TESYFSMDGD 161

RESULT 15
US-10-467-657-6894
; Sequence 6894, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 11:21:24 ; Search time 186 Seconds
(without alignments)
99.215 Million cell updates/sec

Title: US-10-763-276-7_COPY_1154_1195
Perfect score: 208
Sequence: 1 SELVEHLGNLQNAQQDGK.....IVLPISETLSMEEDSGLSLP 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	208	100.0	1306	8 ADQ39807	Adq39807 Human myo
3	208	100.0	1354	9 ADZ00446	Adz00446 VEGFR-2.
4	208	100.0	1355	2 AAW80997	Aaw80997 Human rec
5	208	100.0	1356	2 AAR26999	Aar26999 Novel typ
6	208	100.0	1356	2 AAW59275	Aaw59275 Human KDR
7	208	100.0	1356	2 AAB62475	Aab62475 Human VEG
8	208	100.0	1356	4 AAY97783	Aay97783 Human KDR
9	208	100.0	1356	4 AAY97576	Aay97576 Human Flk
10	208	100.0	1356	5 AAU79427	Aau79427 Human Kin
11	208	100.0	1356	5 AAU79429	Aau79429 Human Kin
12	208	100.0	1356	5 AAU79426	Aau79426 Human Kin
13	208	100.0	1356	5 ABR40196	Abr40196 Human vas
14	208	100.0	1356	7 ADD08954	Add08954 Human VEG
15	208	100.0	1356	7 ABM79007	Abm79007 Human VEG
16	208	100.0	1356	7 ADF45097	Adf45097 Human kin
17	208	100.0	1356	7 ABU64302	Abu64302 Human KDR
18	208	100.0	1356	8 ADH17130	Adh17130 Human vas
19	208	100.0	1356	8 ADG70543	Adg70543 Human KDR
20	208	100.0	1356	8 ADQ39806	Adq39806 Human myo
21	208	100.0	1356	8 ADQ39808	Adq39808 Human myo
22	208	100.0	1356	8 ADRA4648	Adra4648 Cancer-as
23	208	100.0	1356	8 ADT92353	Adt92353 Human vas
24	208	100.0	1356	9 ADV90285	Adv90285 Protease-

25	208	100.0	1356	9 ADY59385	Ady59385 Human VEG
26	208	100.0	1356	9 ADZ26561	Adz26561 Human VEG
27	205	98.6	558	8 ADR32352	Adr32352 Rat recep
28	205	98.6	820	8 ADR32354	Adr32354 GST-rat K
29	205	98.6	1343	8 ADR32351	Adr32351 Rat recep
30	205	98.6	1343	8 ADR32338	Adr32338 Rat optim
31	205	98.6	1345	7 ABM79009	Abm79009 Murine Fl
32	205	98.6	1367	2 AAR28041	Aar28041 flk-1. 3/
33	205	98.6	1367	2 AAR31377	Aar31377 Human flk
34	205	98.6	1367	2 AAR37504	Aar37504 Murine fl
35	205	98.6	1367	2 AAR44996	Aar44996 Murine fl
36	205	98.6	1367	2 AAR54046	Aar54046 Sequence
37	205	98.6	1367	2 AAR67537	Aar67537 Mouse flk
38	205	98.6	1367	2 AAR67817	Aar67817 Flkl rece
39	205	98.6	1367	2 AAR97420	Aar97420 Murine fo
40	205	98.6	1367	2 AAW19875	Aaw19875 Murine fl
41	205	98.6	1367	2 ADP90725	Adp90725 Mouse foe
42	205	98.6	1367	2 AAY08618	Aay08618 Murine fl
43	205	98.6	1367	5 ABG70917	Abg70917 Mouse rec
44	205	98.6	1367	5 AAE25820	Aae25820 Murine re
45	205	98.6	1367	6 ABR40197	Abr40197 Murine va

ALIGNMENTS

RESULT 1
ADY85472
ID ADY85472 standard; protein; 429 AA.
XX
AC ADY85472;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein VEGFR.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
XX neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
(PLEX-) PLEXIKON INC.
XX
PA Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RU;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
XX protein kinases and treating kinase associated disorders e.g. cancer,
XX comprises set of compounds comprising N-heterocyclic compounds.
XX
XX Disclosure; Page 170-174; 236pp; English.

XX The invention relates to a new kinase scaffold library comprises at least
XX 1 set of compounds, each set comprising at least 1 N-heterocyclic
XX compound of formulae (I)-(VII) given in the specification. Also included
XX are a system for fitting compounds in binding sites of protein kinases
XX (comprising an electronic kinase scaffold, and a scaffold library
XX comprising at least 1 collection of electronic representations of (I)-
XX (VII), where the scaffold library is embedded in a computer device and
XX the electronic representations of the compounds can be selectively
XX retrieved and functionally connected with computer software adapted to
XX fit electronic representations of compounds in an electronic
XX representation of a binding site of a kinase), obtaining improved ligands

CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group), and developing a ligand for a kinase
CC comprising conserved residues matching at least one of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.

XX SQ Sequence 429 AA;

Query Match 100.0%; Score 208; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 2.2e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

DB 371 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 412

RESULT 2

ADQ39807

ID ADQ39807 standard; protein; 1306 AA.

XX ADQ39807;

XX 18-NOV-2004 (first entry)

XX Human myocardial infarction-associated gene derived protein, SEQ ID 1470.
DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiant; gene therapy; human.

KW Homo sapiens.

OS WO2004058052-A2.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

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XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX (APPL-) APPLERA CORP.

XX Cargill M, Devlin JJ, Iakoubova O;

PI WPI; 2004-533949/51.

XX N-PSDB; ADQ38979.

DR Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX Claim 10; SEQ ID NO 1470; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 1306 AA;

Query Match 100.0%; Score 208; DB 8; Length 1306;

Best Local Similarity 100.0%; Pred. No. 9.5e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

DB 1104 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1145

RESULT 3

ADZ00446

ID ADZ00446 standard; protein; 1354 AA.

XX ADZ00446;

XX 16-JUN-2005 (first entry)

XX VEGFR-2.

XX

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XX

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XX

KW neotropilin-2; VEGF-C deltaC156; heparin-binding VEGF-C;
 KW neurotherapeutic; interferon gamma; nerve growth factor;
 KW epidermal growth factor; EGF; basic fibroblast growth factor; bFGF;
 KW neurogenin; brain derived neurotrophic factor; BDNF; thyroid hormone;
 KW bone morphogenic protein; BMP; leukemia inhibitory factor; LIF;
 KW sonic hedgehog; glial cell line-derived neurotrophic factor; GDNF;
 KW vascular endothelial growth factor; VEGF; interleukin; interferon;
 KW stem cell factor; SCF; activin; inhibin; chemokine; retinoic acid;
 KW ciliary neurotrophic factor; CNTF; tacrine; Cognex; donepezil; Aricept;
 KW rivastigmine; Exelon; galantamine; Reminyl; cholinesterase inhibitor;
 KW anti-inflammatory; anti-cholinergic; dopamine agonist;
 KW catechol-O-methyl-transferase; COMT; amantadine; Symmetrel; Sinemet;
 KW Selegiline; carbidopa; ropinirole; Requip; coenzyme Q10; Pramipexole;
 KW Mirapex; levodopa; L-dopa; Alzheimers disease; Parkinsons disease;
 KW Huntingtons disease; motor neuron disease;
 KW Amyotrophic lateral Sclerosis; ALS; dementia; cerebral palsy;
 KW demyelination; multiple sclerosis; phenylketonuria;
 KW periventricular leukomalacia; PVL; HIV-1 encephalitis; HIVE;
 KW Guillian Barre Syndrome; GBS;
 KW acute inflammatory demyelinating polynuropathy; AIDP;
 KW acute motor axonal neuropathy; AMAN;
 KW acute motor sensory axonal neuropathy; AMSAN; Fisher syndrome;
 KW acute pandysautonomia;
 KW chronic inflammatory demyelinating polyradiculoneuropathy; CIDP;
 KW multifocal acquired demyelinating sensory and motor neuropathy; MADSAM;
 KW Lewis-Sumner syndrome;
 KW distal acquired demyelinating symmetric neuropathy; DADS; neural trauma;
 KW neural injury; stroke; spinal cord injury; post-operative injury;
 KW brain ischemia; neuroblastoma; neural tumor.
 XX Homo sapiens.
 OS
 XX
 PN WO2005030240-A2.
 XX
 PD 07-APR-2005.
 XX
 PF 23-SEP-2004; 2004WO-US031318.
 XX
 PR 23-SEP-2003; 2003US-00669176.
 PR 23-SEP-2003; 2003US-0505607P.
 XX
 PA (LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Alitalo K, Karkainen M, Haiko P, Sainio K, Wartiovaara K;
 PI Thomas JL, Eichmann A;
 XX
 XX WPI; 2005-273287/28.
 DR N-PSDB; AD200445.
 DR GENBANK; L04947.
 XX

XX Use of a vascular endothelial growth factor-C or -D product in
 PT medicaments for promoting growth and differentiation of neural stem cells
 PT for neurodegenerative disorders such as Alzheimer's and Parkinson's
 PT disease.

XX Disclosure; SEQ ID NO 28; 263pp; English.

XX This sequence represents VEGFR-2. The method of the invention uses a
 CC vascular endothelial growth factor-C (VEGF-C) product or a vascular
 CC endothelial growth factor D (VEGF-D) product in the manufacture of a
 CC medicament to promote recruitment, proliferation, differentiation,
 CC migration or survival of neural cells or neural precursor cells. The
 CC method of the invention comprises identifying a mammalian subject in need
 CC of treatment to promote recruitment, proliferation, differentiation,
 CC migration, or survival of neural cells or neural precursor cells, and
 CC administering to the subject a composition comprising a VEGF-C or VEGF-D
 CC product. The product is a VEGF-C product comprising a purified mammalian
 CC prepro-VEGF-C polypeptide or its fragment that binds VEGFR-3 or
 CC neotropilin-2, a VEGF-C deltaC156 polypeptide, or a chimeric heparin-
 CC binding VEGF-C polypeptide. The method also comprises administering to
 CC the mammalian subject a neurotherapeutic agent, and including in the

CC medicament a neurotherapeutic agent. The neurotherapeutic agent comprises
 CC a neural growth factor and/or a polynucleotide encoding a neural growth
 CC factor selected from interferon gamma, nerve growth factor, epidermal
 CC growth factor (EGF), basic fibroblast growth factor (bFGF), neurogenin,
 CC brain derived neurotrophic factor (BDNF), thyroid hormone, bone
 CC morphogenic proteins (BMPs), leukemia inhibitory factor (LIF), sonic
 CC hedgehog, glial cell line-derived neurotrophic factor (GDNFs), vascular
 CC endothelial growth factor (VEGF), interleukins, interferons, stem cell
 CC factor (SCF), activins, inhibins, chemokines, retinoic acid and ciliary
 CC neurotrophic factor (CNTF). The neurotherapeutic agent is also tacrine
 CC (Cognex), donepezil (Aricept), rivastigmine (Exelon), galantamine
 CC (Reminyl), cholinesterase inhibitors or anti-inflammatory drugs and/or
 CC is anti-cholinergics, dopamine agonists, catechol-O-methyl-transferases
 CC (COMTs), amantadine (Symmetrel), Sinemet (RPM), Selegiline, carbidopa,
 CC ropinirole (Requip), coenzyme Q10, Pramipexole (Mirapex) and levodopa (L-
 CC dopa). The medicament of the invention is for the treatment of a disease
 CC or condition characterized by aberrant growth of neuronal cells, neuronal
 CC scarring, or neural degeneration, or for treatment of neural degeneration
 CC caused by a neurodegenerative disorder selected from the group consisting
 CC of is Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC motor neuron disease, Amyotrophic Lateral Sclerosis (ALS), dementia and
 CC cerebral palsy, and for treatment of a disease or condition with aberrant
 CC growth of oligodendrocyte or oligodendrocyte precursor cells, where the
 CC condition has demyelination in the nervous system. The medicament is also
 CC for the treatment of multiple sclerosis, phenylketonuria, periventricular
 CC leukomalacia (PVL), HIV-1 encephalitis (HIVE), Guillian Barre Syndrome
 CC (GBS), acute inflammatory demyelinating polynuropathy (AIDP), acute
 CC motor axonal neuropathy (AMAN), acute motor sensory axonal neuropathy
 CC (AMSAN), Fisher syndrome, acute pandysautonomia, and Krabbe's disease.
 CC The medicament can also be used for the treatment of chronic inflammatory
 CC demyelinating polyradiculoneuropathy (CIDP), such as multifocal acquired
 CC demyelinating sensory and motor neuropathy (MADSAM, also know as Lewis-
 CC Sumner syndrome) and distal acquired demyelinating symmetric neuropathy
 CC (DADS), and for the treatment of neural trauma or neural injury, where
 CC the neural trauma is a stroke-related injury, spinal cord injury, post-
 CC operative injury or brain ischemia. The VEGF-C inhibitor is useful in the
 CC manufacture of a medicament for the treatment of a neuroblastoma or
 CC neural tumor. The methods and compositions of the present invention are
 CC also useful for cellular and molecular biology and medicine, in
 CC particular for the vascularization and angiogenesis and the interactions
 CC of the vascular system with the nervous system.

XX Sequence 1354 AA;

Query Match 100.0%; Score 208; DB 9; Length 1354;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISFTLSMEEDSGLSLP 42
 |||||
 DB 1152 SELVEHLGNLQANAQQDGKDYIVLPISFTLSMEEDSGLSLP 1193

RESULT 4
 AAW80997
 ID AAW80997 standard; protein; 1355 AA.
 XX
 XX AAW80997;

DT 12-APR-1999 (first entry)

XX Human receptor tyrosine kinase KDR.

XX KDR; receptor tyrosine kinase; human; signal transduction; mitogen;
 KW neovascularization; angiogenesis; diabetic retinopathy; breast cancer;
 KW brain cancer; inflammation; rheumatoid arthritis; psoriasis;
 KW contact dermatitis; hypersensitivity; antagonist; therapy.

XX Homo sapiens.

OS Location/Qualifiers

FH Key 780..1386

FT Domain

FT /note= "intracellular domain, from about amino acid 780-

FT XX 795 to about amino acid 1175-1386"

XX PN WO9858053-A1.

XX PD 23-DEC-1998.

XX PF 17-JUN-1998; 98WO-US012569.

XX PR 18-JUN-1997; 97US-0050962P.

XX PA (MERI) MERCK & CO INC.

XX PI Kendall RL, Thomas KA, Mao X, Tebben A;

XX DR WPI; 1999-095333/08.

XX DR N-PSDB; AAV99829.

XX PT Human receptor tyrosine kinase protein, KDR - useful e.g. to screen for

XX PT antagonists useful to treat diseases involving neoangiogenesis e.g.

XX PT diabetic retinal vascularization, cancers.

XX PS Claim 2; Fig 2; 69pp; English.

XX CC This is the amino acid sequence of a novel receptor tyrosine kinase,

XX CC termed KDR, that is expressed on human endothelial cells. KDR is

XX CC activated by vascular endothelial growth factor and mediates a mitogenic

XX CC signal. It is implicated in clinical neoangiogenesis. The amino acid

XX CC sequence was deduced from an isolated KDR cDNA (see AAV99829). The

XX CC predicted sequence has differences from the previously published KDR

XX CC sequence at positions 498 (Ala to Glu), 772 (Thr to Ala), 787 (Gly to

XX CC Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347 (Thr to Ser), producing

XX CC a protein predicted by computer modeling to have higher activity and

XX CC functionality. The invention also relates to recombinant vectors and

XX CC recombinant hosts which contain a DNA fragment encoding human KDR, a DNA

XX CC fragment encoding the intracellular portion of KDR with or without a

XX CC membrane anchor sequence, purified forms of associated human KDR, and

XX CC human mutant forms of KDR. KDR, fusion proteins or fragments can be used

XX CC in assays to identify antagonists and agonists of human KDR (Claimed).

XX CC Antagonists of KDR useful for treating diseases involving neoangiogenesis

XX CC e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.)

XX CC and forms of inflammation e.g. rheumatoid arthritis, psoriasis, contact

XX CC dermatitis and hypersensitivity reactions. The protein is also useful for

XX CC produce antibodies that can be used to measure human KDR levels and/or

XX CC activity

XX SQ Sequence 1355 AA;

Query Match 100.0%; Score 208; DB 2; Length 1355;

Best Local Similarity 100.0%; Pred. No. 1e-20;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

Db 1153 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1194

RESULT 5

ID AAR26999

XX AAR26999 standard; protein; 1356 AA.

XX AC AAR26999;

XX XX

XX 23-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX XX

DE Novel type III RTK encode by the KDR gene.

XX Receptor tyrosine kinase; vascular endothelial cell growth factors;

KW cancer; tumour; diagnosing; monitoring.

KW

OS Homo sapiens.

OS Unidentified.

XX PH Location/Qualifiers

FT 1. .763

FT /note= "putative extracellular region - contains 21

FT cysteine residues"

FT 46

FT /note= "potential N linked glycosylation site"

FT 66

FT /note= "potential N-linked glycosylation site"

FT 96

FT /note= "potential N-linked glycosylation site"

FT 143

FT /note= "potential N-linked glycosylation site"

FT 158

FT /note= "potential N-linked glycosylation site"

FT 245

FT /note= "potential N-linked glycosylation site"

FT 318

FT /note= "potential N-linked glycosylation site"

FT 374

FT /note= "potential N-linked glycosylation site"

FT 395

FT /note= "potential N-linked glycosylation site"

FT 511

FT /note= "potential N-linked glycosylation site"

FT 523

FT /note= "potential N-linked glycosylation site"

FT 580

FT /note= "potential N-linked glycosylation site"

FT 613

FT /note= "potential N-linked glycosylation site"

FT 631

FT /note= "potential N-linked glycosylation site"

FT 675

FT /note= "potential N-linked glycosylation site"

FT 704

FT /note= "potential N-linked glycosylation site"

FT 764. .788

FT /note= "putative membrane spanning region"

FT 868

FT /note= "ATP binding site"

XX WO9214748-A1.

XX 03-SEP-1992.

XX 20-FEB-1992; 92WO-US001300.

XX 22-FEB-1991; 91US-00657236.

XX (AMCY) AMERICAN CYANAMID CO.

XX Terman BI, Carrion ME;

XX WPI; 1992-316117/38.

XX N-PSDB; AAQ28272.

XX DNA encoding type III receptor tyrosine kinase - useful for diagnosing

XX the onset of cancer.

XX Claim 3; Fig 7; 101pp; English.

XX This sequence represents a novel type III receptor tyrosine kinase

XX encoded by the KDR gene. It was decoded from the appropriate cDNA, and

XX its predicted amino acid sequence contains several features which

XX demonstrate that the novel gene is a type III RTK. A hydropathy plot of

XX the predicted amino acid sequence indicates a single membrane spanning

XX region. The putative amino terminal 762 amino acids of the receptor has

XX structural features of extracellular receptor ligand binding domains,

XX including regularly spaced cysteines, and 18 potential N-linked

XX glycosylation sites. The predicted amino acid sequence of the COOH

XX terminal 530 amino acid portion contains an ATP binding site at lysine

XX 868, 22 amino acids downstream from the consensus ATP recognition

CC sequence. Within the kinase domain there is a 55-60% identical match in
CC amino acid sequence to 3 other type III receptor tyrosine kinases: ckit
CC proto-oncogene, CSF-1 and PDGF. The predicted kinase domain contains a
CC kinase insert domain of approximately 71 amino acids, sharing little
CC homology with other type III RTKs. (Updated on 25-MAR-2003 to correct PN
CC field.)

CC Revised record issued on 23-SEP-2004 : Correction to Feature Table Key

XX Sequence 1356 AA;

SQ Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 6

AAW59275 ID AAW59275 standard; protein; 1356 AA.

XX AC AAW59275;

XX DT 27-AUG-1998 (first entry)

XX DE Human KDR protein.

XX KW Kinase insert domain containing receptor; KDR; screening; inhibitor;
KW vascular endothelial growth factor; VEGF; angiogenesis; treatment;
KW cancer.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 45
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 66
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 96
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 143
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 158
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 245
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 318
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 374
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 395
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 511
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 580
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 613
FT /label= N-glycosylated
FT /note= "putative"

FT Modified-site 631
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 675
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 704
FT /label= N-glycosylated
FT /note= "putative"
FT Modified-site 721
FT /label= N-glycosylated
FT /note= "putative"
FT Region 765..789
FT /note= "putative membrane spanning region"
XX US5766860-A.
XX PD 16-JUN-1998.
XX PF 25-FEB-1997; 97US-00810116.
XX PR 23-NOV-1992; 92US-00930548.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Terman BI, Carrion ME;
XX DR WPI, 1998-361682/31.
XX DR N-PSDB; AAV34763.
XX PT Screening assay for vascular endothelial cell growth factor antagonists -
XX using recombinant cells expressing receptor protein.
XX PS Claim 1; Fig 7A-M; 5lpp; English.
XX CC This sequence represents a novel human growth factor receptor, kinase
CC insert domain containing receptor or KDR. This receptor is capable of
CC binding to the vascular endothelial cell growth factor, VEGF and is used
CC in a screening assay which identifies compounds that inhibit VEGF action
CC on KDR. Such compounds which inhibit binding of VEGF to the KDR may
CC inhibit angiogenesis and thus be useful for treating cancer
XX SQ Sequence 1356 AA;
Query Match 100.0%; Score 208; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 7
AAB62475 ID AAB62475 standard; protein; 1356 AA.
XX AC AAB62475;
XX DT 09-JUL-2001 (first entry)
XX DE Human VEGFR-2 receptor protein.
XX KW Receptor protein; vascular endothelial growth factor receptor-2; VEGFR-2;
XX neuropilin-1; NP-1; co-receptor; human; angiogenic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Domain 1..760
FT /note= "extracellular domain"
FT Domain 124..320
FT /note= "Ig domain"

```

XX WO200131346-A2.
XX
XX 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-US029579.
XX
XX PR 28-OCT-1999; 99US-0162367P.
XX
XX PA (PROC ) PROCTER & GAMBLE CO.
XX
XX P1 Rosenbaum JS, Whitaker GB, Limberg BJ;
XX
XX WPI; 2001-308686/32.
XX
XX DR N-PSDB; AAF83308.
XX
XX PT Determining compounds which bind to a complex comprising vascular
XX endothelial growth factor receptor-2 and Neuropllin-1 to provide superior
XX pro- and anti-angiogenic agents.
XX
XX PS Claim 7; Page 32-39; 82pp; English.
XX
XX CC The invention relates to determining whether a compound is capable of
XX binding to a receptor protein complex comprising a vascular endothelial
XX growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
XX (NP-1) receptor protein. One method comprises introducing a sample
XX comprising the compound to the receptor protein and allowing the compound
XX to bind to the complex. Signaling through VEGFR-2 is enhanced in the
XX presence of the NP-1 co-receptor. The methods of the invention can be
XX used for identifying novel pro- and anti-angiogenic compounds. The
XX present sequence represents the human VEGFR-2 receptor protein
XX
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLQANAQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 9
AA97576
ID AA97576 standard; protein; 1356 AA.
XX
XX AC AA97576;
XX
XX DT 05-APR-2001 (first entry)
XX
XX DE Human Flk-1 transmembrane and extracellular domains.
XX
XX KW Human; angiogenic protein; wound healing; vascular tissue repair;
XX peripheral arterial disease; critical limb ischaemia; coronary disease;
XX angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
XX rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
XX infectious disease; neurodegeneration; Flk-1.
XX
XX OS Homo sapiens.
XX
XX PN WO200075163-A1.
XX
XX PD 14-DEC-2000.
XX
XX PF 01-JUN-2000; 2000WO-US014925.
XX
XX PR 03-JUN-1999; 99US-0137796P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM, Hu J, Cao L;
XX
XX WPI; 2001-071057/08.
XX
XX PT New nucleic acid encoding angiogenic proteins, useful e.g. for promoting
XX healing of wounds and treating peripheral arterial disease, critical limb
XX ischemia or coronary disease.
XX
XX PS Example 48; Page 236-240; 244pp; English.
XX
XX CC This sequence is a human Flk-1 fragment, and was used in the isolation of
XX an angiogenic protein of the invention. The angiogenic proteins and the
XX DNA sequences encoding them, are used to prevent, treat or ameliorate
XX disease and to detect diseases, or susceptibility, by detecting mutations
XX

```


or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic (antagonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide range of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating regeneration of the nervous system

XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 10

AAU79427
ID AAU79427 standard; protein; 1356 AA.

AC AAU79427;

XX 02-JUL-2002 (first entry)

DE Human Kinase insert domain-containing receptor mutant Y801P.

XX Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
KW fetal liver kinase-1; cytosolic; antidiabetic; antirheumatic; mutein;
KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
XX angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 801 /note= "Wild-type Tyr substituted by Phe"

XX WO200229090-A1.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-JP008684.

XX 03-OCT-2000; 2000JP-00303694.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA (SHIB/) SHIBUYA M.

XX Shibuya M, Takahashi T, Furuya A, Shitara K;

XX WPI; 2002-352237/38.

XX Screening substances inhibiting the binding of signal-transducing
PT molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT of e.g. tumor.

XX Example 8; Page; 81pp; Japanese.

PS The invention relates to inhibiting the signal transduction of KDR/Flk-1
XX (kinase insert domain-containing receptor/fetal liver kinase-1) is by
CC using a substance inhibiting the binding of a signal-transducing molecule
CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
CC included are methods of detecting/inhibiting/screening for cell
CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
CC phosphorylation at tyrosine at the 1175-position using the binding
CC inhibitors, compounds obtained by the screening methods, drugs containing
CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-1
CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
CC monoclonal antibody or its fragment, a recombinant vector containing the
CC DNA and a transformant obtained by transferring the recombinant vector
CC into a host cell. The method is useful for screening substances
CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
CC phosphorylated at tyrosine at 1175-position, as cell proliferation
CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
CC detecting angiogenesis is also provided. The present sequence is the
CC Human KDR/FLK-1 mutant where Tyr at 801 is replaced by Phe. Note: The
CC present sequence is not shown in the specification but was created by the
CC indexer using the KDR/FLK-1 sequence appearing as AAU74926 and the
CC information in example 8

XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||

DB 1154 SELVEHLGNLQANAAQDGKDYIVLPISETLSMEEDSGLSLP 1195
|||||

RESULT 11

AAU79429

ID AAU79429 standard; protein; 1356 AA.

XX AC AAU79429;

XX 02-JUL-2002 (first entry)

XX Human Kinase insert domain-containing receptor mutant Y1214F.

XX Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
KW fetal liver kinase-1; cytosolic; antidiabetic; antirheumatic; mutein;
KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
XX angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1214 /note= "Wild-type Tyr substituted by Phe"

XX WO200229090-A1.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-JP008684.

XX 03-OCT-2000; 2000JP-00303694.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA (SHIB/) SHIBUYA M.

XX Shibuya M, Takahashi T, Furuya A, Shitara K;

XX WPI; 2002-352237/38.

XX Screening substances inhibiting the binding of signal-transducing
 PT molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
 PT cell proliferation inhibitors and angiogenesis inhibitors for treatment
 PT of e.g. tumor.
 XX
 PS Example 8; Page; 81pp; Japanese.
 XX
 CC The invention relates to inhibiting the signal transduction of KDR/Flk-1
 CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
 CC using a substance inhibiting the binding of a signal-transducing molecule
 CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
 CC included are methods of detecting/inhibiting/screening for cell
 CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
 CC phosphorylation at tyrosine at the 1175-position using the binding
 CC inhibitors, compounds obtained by the screening methods, drugs containing
 CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk
 CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
 CC monoclonal antibody or its fragment, a recombinant vector containing the
 CC DNA and a transformant obtained by transferring the recombinant vector
 CC into a host cell. The method is useful for screening substances
 CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
 CC phosphorylated at tyrosine at 1175-position, as cell proliferation
 CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
 CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
 CC detecting angiogenesis is also provided. The present sequence is the
 CC Human KDR/Flk-1 mutant where Tyr at 1214 is replaced by Phe. Note: The
 CC present sequence is not shown in the specification but was created by the
 CC indexer using the KDR/Flk-1 sequence appearing as AAU74926 and the
 CC information in example 8

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 5; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||
 DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 12
 AAU79426
 ID AAU79426 standard; protein; 1356 AA.

XX AC AAU79426;

XX DT 02-JUL-2002 (first entry)

XX DE Human Kinase insert domain-containing receptor.

XX KW Human; KDR; kinase insert domain-containing; receptor; Flk-1;
 KW fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic;
 KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
 KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.

XX OS Homo sapiens.

XX PN WO200229090-A1.

XX PD 11-APR-2002.

XX PF 02-OCT-2001; 2001WO-JP008684.

XX PR 03-OCT-2000; 2000JP-00303694.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PA (SHIB/) SHIBUYA M.

XX PI Shibuya M, Takahashi T, Furuya A, Shitara K;

XX WPI; 2002-352237/38.

XX Screening substances inhibiting the binding of signal-transducing
 PT molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
 PT cell proliferation inhibitors and angiogenesis inhibitors for treatment
 PT of e.g. tumor.
 XX

PS Disclosure; Page 65-71; 81pp; Japanese.

XX The invention relates to inhibiting the signal transduction of KDR/Flk-1
 CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
 CC using a substance inhibiting the binding of a signal-transducing molecule
 CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
 CC included are methods of detecting/inhibiting/screening for cell
 CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
 CC phosphorylation at tyrosine at the 1175-position using the binding
 CC inhibitors, compounds obtained by the screening methods, drugs containing
 CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk
 CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
 CC monoclonal antibody or its fragment, a recombinant vector containing the
 CC DNA and a transformant obtained by transferring the recombinant vector
 CC into a host cell. The method is useful for screening substances
 CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
 CC phosphorylated at tyrosine at 1175-position, as cell proliferation
 CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
 CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
 CC detecting angiogenesis is also provided. The present sequence is the
 CC Human KDR/Flk-1 protein

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 5; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
 |||||
 DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 13
 ABR40196

ID ABR40196 standard; protein; 1356 AA.

XX AC ABR40196;

XX DT 01-AUG-2003 (first entry)

XX DE Human vascular endothelial growth factor receptor-2.

XX KW Human; vascular endothelial growth factor receptor-2; cytostatic;
 KW angiogenic; antiangiogenic; antiarthritic; antirheumatic; antisense;
 KW VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis;
 KW angiogenesis.

XX OS Homo sapiens.

XX PN WO2003029266-A1.

XX PD 10-APR-2003.

XX PF 26-SEP-2002; 2002WO-US030734.

XX PR 28-SEP-2001; 2001US-00967655.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Watt AT;

XX WPI; 2003-371980/35.

XX DR N-PSDB; ACC71713.

XX PT New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding vascular endothelial growth factor receptor-2

PT (VEGFR-2), useful for treating a disease/condition associated with VEGFR-2, e.g. cancer.

XX Example 13; Page 90-97; 127pp; English.

XX The present invention relates to novel antisense oligonucleotides (ACC71728-ACC71750 and ACC80101-ACC80155) targeted to Vascular Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and CC which inhibit the expression of VEGFR-2. The oligonucleotides are useful CC in compositions for treating a disease or condition associated with VEGFR CC -2, such as hyperproliferative disorder, e.g. cancer, a disease or CC condition involving angiogenesis, or rheumatoid arthritis. The present CC sequence is human VEGFR-2

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 6; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
|||||
DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 14

ID ADD08954 standard; protein; 1356 AA.

AC ADD08954;

XX 01-JAN-2004 (first entry)

DE Human VEGFR-2 protein SEQ ID NO:30.

XX screening; modulator; binding; neuropilin growth factor receptor;
KW vascular endothelial growth factor C;
KW vascular endothelial growth factor receptor 3; VEGF-C; VEGFR-3;
KW neuropilin; cytosolic; neurotrophic; neuroprotective; vulnary;
KW vasotrophic; cardiant; angiogenic process; nervous system growth;
KW nervous system function; cancer; ischaemia; cerebral infarction;
KW cerebral bleeding; Alzheimer's disease; myocardial infarction; human.

XX Homo sapiens.

XX WO2003029814-A2.

XX 10-APR-2003.

XX 01-OCT-2002; 2002WO-EP0111069.

XX 01-OCT-2001; 2001US-0326326P.

XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.

XX Alitalo K, Karkkainen M, Karila K;

XX WPI; 2003-381660/36.

XX N-PSDB; ADD08953.

PT Screening for modulators of neuropilin and vascular endothelial growth
PT factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction
PT of neuropilin and VEGF-C or VEGFR-3 in the presence and absence of a
PT modulator compound.

XX Disclosure; SEQ ID NO 30; 181pp; English.

XX The present invention describes a method of screening for modulators of
CC binding between a neuropilin growth factor receptor and a vascular
CC endothelial growth factor (VEGF)-C or VEGFR-3 polypeptide comprising
CC comparing the binding between neuropilin and VEGF-C or VEGFR-3 in the
CC presence and in the absence of a putative modulator compound. Also

CC described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR-3 or neuropilin biological activity; (2) modulating growth, migration or CC proliferation of cells in a mammalian organism; (3) a bispecific antibody CC which specifically binds to a neuropilin receptor and a VEGF-C or VEGFR-3 CC polypeptide; (4) modulating neuronal growth or neuronal scarring in a CC mammalian organism; and (5) a polypeptide comprising a fragment of a VEGF CC -C that binds to a neuropilin receptor. The modulators have cytostatic, CC activities. The method is useful in modulating angiogenic processes and CC nervous system growth and function, such as in the treatment of cancer, CC wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or CC myocardial infarction. The polypeptide comprising a fragment of a VEGF-C CC that binds to a neuropilin receptor, is useful for manufacturing a CC medicament for the treatment of diseases characterised by aberrant CC growth, migration or proliferation of cells that express a neuropilin CC receptor. The present sequence represents human VEGFR-2, which is used in CC the exemplification of the present invention.

XX Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 7; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42

DB 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 15

ABM79007

ID ABM79007 standard; protein; 1356 AA.

XX AC ABM79007;

XX 15-JAN-2004 (first entry)

XX Human VEGF receptor-2 (KDR).

XX Human; vascular endothelial growth factor receptor-2; VEGFR-2; KDR;
KW receptor; vaccine; genetic immunisation; gene therapy; cytostatic.

XX Homo sapiens.

XX WO2003073995-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006256.

XX 02-MAR-2002; 2002US-00090183.

XX (SCRI) SCRIPPS RES INST.

XX Reisfeld RA, Niethammer AG, Xiang R;

XX WPI; 2003-756753/71.

XX N-PSDB; ACF80601.

XX New DNA vaccine for eliciting an immune response against proliferating
PT endothelial cells comprising a DNA construct operably encoding a VEGF
PT receptor protein in a carrier, useful for inhibiting tumor growth or
PT angiogenesis.

XX Claim 3; Fig 2; 56pp; English.

XX The present sequence is the protein sequence of human vascular

CC endothelial growth factor receptor-2 (VEGFR2 or KDR). A claimed DNA
CC vaccine effective for eliciting an immune response against proliferating
CC endothelial cells comprises a DNA construct operably encoding a VEGF
CC receptor protein (e.g. KDR) in a carrier. The DNA construct may be a
CC naked DNA construct or incorporated into a plasmid vector or into an
CC attenuated bacterial vector such as attenuated Salmonella typhimurium.

```
CC The DNA vaccine is used in claimed methods of inhibiting endothelial cell
CC proliferation, inhibiting angiogenesis, and inhibiting tumour growth
SQ Sequence 1356 AA;

Query Match      100.0%; Score 208; DB 7; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
   |||||
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 16
ADF45097
ID ADF45097 standard; protein; 1356 AA.
XX
AC ADF45097;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase VEGFR2.
XX
KW Human; protein kinase; enzyme; inhibitor; VEGFR2.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 66; 260pp; English.
XX
CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 1356 AA;

Query Match      100.0%; Score 208; DB 7; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
   |||||
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 17
ABU64302
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```
ID ABU64302 standard; protein; 1356 AA.
XX
AC ABU64302;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human KDR protein.
XX
KW Vector; rAAV; recombinant adeno-associated viral vector;
KW anti-angiogenesis; PEDF; angiogenesis; eye disorder; blindness;
KW retinal degeneration; macular degeneration; neovascularisation;
KW ophthalmological.
XX
OS Homo sapiens.
XX
PN WO2003080648-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008667.
XX
PR 20-MAR-2002; 2002US-0366114P.
XX
PA (UYFL ) UNIV FLORIDA RES FOUND INC.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Hauswirth WM, Campochiaro PA, Berns KI;
XX
WPI; 2003-779243/73.
XX
DR N-PSDB; AAL56271.
XX
PT Novel adeno-associated viral vector comprising polynucleotide encoding
PT pigment epithelium-derived factor, useful for treating choroidal
PT neovascularization, blindness, loss of vision.
XX
PS Claim 14; Page 50-51; Opp; English.
XX
CC The present invention relates to an adeno-associated viral (AAV) vector
CC comprising a polynucleotide that comprises a nucleic acid segment that
CC encodes a choroidal or ocular neovascularisation inhibitory polypeptide
CC operably linked to a promoter that expresses the segment to produce the
CC polypeptide in a selected mammalian host cell. Such a vector is useful
CC for providing a choroidal or ocular neovascularisation inhibitory
CC polypeptide to a mammal, for use in the therapy of ocular
CC neovascularisation, choroidal neovascularisation, retinal
CC neovascularisation, age-related macular degeneration, visual impairment,
CC ocular dysfunction, loss of vision, retinopathy, or blindness in a human.
CC The present sequence is a protein shown in the exemplification of the
CC invention
XX
SQ Sequence 1356 AA;

Query Match      100.0%; Score 208; DB 7; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
   |||||
Db 1154 SELVEHLGNLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 18
ADH17130
ID ADH17130 standard; protein; 1356 AA.
XX
AC ADH17130;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human vascular endothelial growth factor receptor 2 (VEGFR2) protein.
XX
KW tyrosine kinase activity; type 1 plasminogen activator inhibitor; PAI-1;
KW TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin;
```

KW vascular endothelial growth factor; VEGF; placental growth factor; PLGF;
KW migration inhibitory factor; MIG; human;
KW vascular endothelial growth factor receptor 2; VEGFR2; receptor.
XX
OS Homo sapiens.
XX WO2003097854-A2.
XX
XX 27-NOV-2003.
XX
XX 19-MAY-2003; 2003WO-US015711.
XX
XX 17-MAY-2002; 2002US-0380872P.
XX 24-FEB-2003; 2003US-0448874P.
XX 24-FEB-2003; 2003US-0448922P.
XX
XX (SUGEN-) SUGEN INC.
XX
XX Morimoto A, Deprimo S, O'farrell A, Smolich BD, Manning WC;
PI Walter SA, Schilling JW, Cherrington J;
XX
XX WPI; 2004-042604/04.
XX
XX Determining whether a test compound inhibits tyrosine kinase activity in
PT a mammal by exposing the mammal to the test compound and measuring in the
PT mammal the level of at least one of the measured proteins or mRNA
PT transcripts.
XX
XX Disclosure; SEQ ID NO 129; 408pp; English.
XX
XX The invention relates to a novel method for determining whether a test
PS compound inhibits tyrosine kinase activity in a mammal comprising
XX measuring in the mammal the level of at least one of the proteins and/or
XX mRNA transcripts or genes for such proteins comprising type 1 plasminogen
XX activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of
XX metalloproteinase 1), vinculin, vascular endothelial growth factor
XX (VEGF), placental growth factor (PLGF), VEGF/PLGF heterodimers or
XX migration inhibitory factor (MIG), exposing the mammal to the test
XX compound and then measuring in the mammal the level of at least one of
XX the proteins and/or mRNA transcripts previously measured. The method of
XX the invention may be useful for determining whether a test compound
XX inhibits tyrosine kinase activity in a mammal. The current sequence is
XX that of the tyrosine kinase activity inhibition-related protein of the
XX invention.
XX
XX Sequence 1356 AA;
SQ
Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLLQANAQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 19
ADG70543
ID ADG70543 standard; peptide; 1356 AA.
XX
XX ADG70543;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human KDR/Flk-1, SEQ ID NO:5.
XX
XX Kinase insert domain-containing receptor; foetal liver kinase-1; KDR;
KW Flk-1; KDR/Flk-1; signal transduction inhibition;
KW tyrosine phosphorylation; phosphospecific antibody; transgenic animal;
KW drug screening; tyrosine phosphorylation inhibitor;
KW angiogenesis detection; angiogenesis inhibition; cell growth inhibition;
KW tumour; cancer; diabetic retinopathy; cytostatic; antidiabetic;
KW ophthalmological; human.

XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 1214
FT /note= "Tyr is optionally O-phosphorylated"
XX
XX JP2003310276-A.
XX
XX 05-NOV-2003.
XX
XX 30-APR-2002; 2002JP-00129072.
XX
XX 30-APR-2002; 2002JP-00129072.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX (SHIB/) SHIBUYA M.
XX
XX WPI; 2004-027148/03.
XX
XX Inhibiting information transmission of kinase insert domain-containing
PT receptor/fms-like tyrosine kinase-1 by a substance that inhibits coupling
PT of information transmission molecules to phosphorylated tyrosines of the
PT kinase.
XX
XX Disclosure; SEQ ID NO 5; 23pp; Japanese.
XX
XX The invention relates to a method of inhibiting signal transduction by
CC kinase insert domain-containing receptor/foetal liver kinase-1 (KDR/Flk-
CC 1) using a substance that inhibits the coupling of a signal transduction
CC molecule to the phosphorylated tyrosine at position 1214 of KDR/Flk-1. The
CC invention also relates to use of KDR/Flk-1 signal transduction inhibitors
CC to inhibit cell growth or angiogenesis; screening for substances which
CC inhibit KDR/Flk-1-mediated signal transduction; the compounds identified;
CC a method of detecting angiogenesis in a tissue; a tyrosine
CC phosphorylation inhibitor that inhibits phosphorylation of tyrosine 1214
CC of KDR/Flk-1; an antibody specific for the phosphorylated form of KDR/Flk-
CC -1; a nucleic acid encoding the antibody; and vectors, host cells and
CC transgenic animals comprising the nucleic acid. Inhibition of KDR/Flk-1-
CC mediated signal transduction is useful for inhibiting angiogenesis and
CC cell growth, which is in turn useful in the treatment of diseases such as
CC tumours and diabetic retinopathy. The present sequence represents human
CC KDR/Flk-1.
XX
XX Sequence 1356 AA;
SQ
Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLLQANAQDGKDYIVLPISETLSMEEDSGLSLP 42
DB 1154 SELVEHLGNLLQANAQDGKDYIVLPISETLSMEEDSGLSLP 1195
RESULT 20
ADQ39806
ID ADQ39806 standard; protein; 1356 AA.
XX
XX ADQ39806;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1469.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiac; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX

```
XX PF 22-DEC-2003; 2003WO-US040978.
XX XX
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX XX
XX PA (APPL-) APPLERA CORP.
XX PI
XX PI Cargill M, Devlin JJ, Iakoubova O;
XX XX
XX DR WPI; 2004-533949/51.
XX DR N-PSDB; ADQ38980.
XX XX
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX XX
XX PS Claim 10; SEQ ID NO 1469; 145pp; English.
XX XX
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiant activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNP's of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 21
ADQ39808
ID ADQ39808 standard; protein; 1356 AA.
XX AC ADQ39808;
XX DT 18-NOV-2004 (first entry)
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1471.
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiant; gene therapy; human.
XX XX
```

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OS Homo sapiens.
XX PN WO2004058052-A2.
XX XX
XX PD 15-JUL-2004.
XX XX
XX PF 22-DEC-2003; 2003WO-US040978.
XX XX
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX XX
XX PA (APPL-) APPLERA CORP.
XX PI
XX PI Cargill M, Devlin JJ, Iakoubova O;
XX XX
XX DR WPI; 2004-533949/51.
XX DR N-PSDB; ADQ38980.
XX XX
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX XX
XX PS Claim 10; SEQ ID NO 1471; 145pp; English.
XX XX
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiant activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNP's of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 1356 AA;

Query Match 100.0%; Score 208; DB 8; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

RESULT 22
AD46648
ID AD46648 standard; protein; 1356 AA.
XX AC AD46648;
XX DT 18-NOV-2004 (first entry)
XX XX
```


XX Disclosure; SEQ ID NO 187; 393pp; English.
PS
XX
CC The invention relates to a method of detecting lineage-specific cells in
CC a biological sample which comprises identifying lineage-specific mRNA in
CC the sample. The methods are useful for determining the clinical outcome
CC of a progenitor cell transfer in a subject, and for identifying or
CC quantifying lineage-specific cells. The present sequence represents the
CC amino acid sequence of a human protein used to identify lineage-specific
CC cells.
XX
SQ Sequence 1356 AA;
Query Match 100.0%; Score 208; DB 9; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 42
Db 1154 SELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLP 1195

Search completed: December 9, 2005, 11:24:37
Job time : 186 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:29:01 ; Search time 2.49057 Seconds
(without alignments)
24.665 Million cell updates/sec

Title: US-10-763-276-1

Perfect score: 62

Sequence: 1 CDGKYIVLPI 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
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5: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	61.3	365	6 US-10-821-234-1575	Sequence 1575, Ap
2	36	58.1	338	6 US-10-821-234-1565	Sequence 1565, Ap
3	36	58.1	358	6 US-10-821-234-1583	Sequence 1583, Ap
4	34	54.8	322	6 US-10-878-556A-16	Sequence 16, Appl
5	34	54.8	1338	6 US-10-821-234-1622	Sequence 1622, Ap
6	34	54.8	1338	7 US-11-109-156-23	Sequence 23, Appl
7	33	53.2	60	7 US-11-091-668-15	Sequence 15, Appl
8	33	53.2	109	6 US-10-467-657-3702	Sequence 3702, Ap
9	33	53.2	478	6 US-10-467-657-3994	Sequence 3994, Ap
10	33	53.2	772	7 US-11-147-238-2	Sequence 2, Appl
11	33	53.2	772	7 US-11-147-238-5	Sequence 5, Appl
12	33	53.2	1133	6 US-10-821-234-1219	Sequence 1219, Ap
13	32	51.6	214	6 US-10-467-657-7796	Sequence 7796, Ap
14	32	51.6	224	7 US-11-000-463-279	Sequence 279, App
15	32	51.6	234	6 US-10-467-657-2238	Sequence 2238, Ap
16	32	51.6	236	7 US-11-000-463-278	Sequence 278, App
17	32	51.6	316	6 US-10-467-657-2250	Sequence 2250, Ap
18	32	51.6	316	6 US-10-467-657-6552	Sequence 6552, Ap
19	32	51.6	319	6 US-10-793-626-2760	Sequence 2760, Ap
20	32	51.6	605	7 US-11-137-465-41	Sequence 41, Appl
21	32	51.6	1683	6 US-10-982-545-6	Sequence 6, Appl
22	31	50.0	114	7 US-11-137-465-52	Sequence 52, Appl
23	31	50.0	182	6 US-10-793-626-2414	Sequence 2414, Ap
24	31	50.0	394	6 US-10-131-826A-520	Sequence 520, App
25	31	50.0	411	6 US-10-793-626-3236	Sequence 3236, App

26 31 50.0 431 7 US-11-060-920-4 Sequence 4, Appli
27 31 50.0 552 6 US-10-793-626-1182 Sequence 1182, Ap
28 718 6 US-10-467-657-8476 Sequence 8476, Ap
29 31 50.0 746 7 US-11-074-176-314 Sequence 314, App
30 31 50.0 747 7 US-11-018-018-1 Sequence 1, Appli
31 31 50.0 747 7 US-11-047-757-1 Sequence 1, Appli
32 31 50.0 749 7 US-11-074-176-54 Sequence 54, Appli
33 31 50.0 944 6 US-10-793-626-3324 Sequence 3324, Ap
34 31 50.0 2828 7 US-11-080-991-54 Sequence 54, Appl
35 31 50.0 2828 7 US-11-186-284-49 Sequence 49, Appl
36 30 48.4 91 6 US-10-467-657-5566 Sequence 5566, Ap
37 30 48.4 245 6 US-10-467-657-4742 Sequence 4742, Ap
38 30 48.4 268 6 US-10-878-556A-46 Sequence 46, Appl
39 30 48.4 311 6 US-10-793-626-3112 Sequence 3112, Ap
40 30 48.4 361 6 US-10-763-712A-122 Sequence 122, App
41 30 48.4 367 6 US-10-793-626-1202 Sequence 1202, Ap
42 30 48.4 379 6 US-10-510-386-76 Sequence 76, Appl
43 30 48.4 382 7 US-11-000-463-447 Sequence 447, App
44 30 48.4 401 7 US-11-110-851-63 Sequence 63, Appl
45 30 48.4 423 7 US-11-110-851-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc SEQ_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 61.3%; Score 38; DB 6; Length 365;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DGKDYIVL 9
DB 143 DGKDYIAL 150

RESULT 2
US-10-821-234-1565
; Sequence 1565, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_seq_genes Version 1.0

; SEQ ID NO 1565

; LENGTH: 338

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-1565

Query Match 58.1%; Score 36; DB 6; Length 338;

Best Local Similarity 75.0%; Pred. No. 6.6;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9

|||||: |

Db 143 DGKDYLL 150

RESULT 3

US-10-821-234-1563

; Sequence 1563, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_seq_genes Version 1.0

; SEQ ID NO 1563

; LENGTH: 358

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-1563

Query Match 58.1%; Score 36; DB 6; Length 358;

Best Local Similarity 75.0%; Pred. No. 7;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9

|||||: |

Db 140 DGKDYLL 147

RESULT 4

US-10-878-556A-16

; Sequence 16, Application US/10878556A

; Publication No. US20050266399A1

; GENERAL INFORMATION:

; APPLICANT: Hoffmann La-Roche Inc.

; TITLE OF INVENTION: HCV regulated protein expression

; FILE REFERENCE: 21762

; CURRENT APPLICATION NUMBER: US/10/878, 556A

; CURRENT FILING DATE: 2004-06-28

; NUMBER OF SEQ ID NOS: 199

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 322

; TYPE: PRT

; ORGANISM: Homo sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: sw_hum/argi_human

; DATABASE ENTRY DATE: 1987-08-13

US-10-878-556A-16

Query Match 54.8%; Score 34; DB 6; Length 322;

Best Local Similarity 70.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CDGKDYIVLP 10

|||||: |

Db 45 CDVKDYGDLP 54

RESULT 5

US-10-821-234-1622

; Sequence 1622, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_seq_genes Version 1.0

; SEQ ID NO 1622

; LENGTH: 1338

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-1622

Query Match 54.8%; Score 34; DB 6; Length 1338;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYI 7

|||||

Db 1165 DGKDYI 1170

RESULT 6

US-11-109-156-23

; Sequence 23, Application US/11109156

; Publication No. US20050250144A1

; GENERAL INFORMATION:

; APPLICANT: Toehio Ota

; APPLICANT: Takao Isogai

; APPLICANT: Tetsuo Nishikawa

; APPLICANT: Koji Hayashi

; APPLICANT: Kaoru Otsuka

; APPLICANT: Jun-Ichi Yamamoto

; APPLICANT: Shizuko Ishii

; APPLICANT: Tomoyasu Sugiyama

; APPLICANT: Ai Wakamatsu

; APPLICANT: Keiichi Nagai

; APPLICANT: Tetsuji Otsuki

; APPLICANT: Shin-Ichi Funahashi

; APPLICANT: Chiaki Senoo

; APPLICANT: Jun-Ichi Nezu

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN

; FILE REFERENCE: PHOSPHATASE

; FILE REFERENCE: 06501-099002

; CURRENT APPLICATION NUMBER: US/11/109,156

; CURRENT FILING DATE: 2005-04-19

; PRIOR APPLICATION NUMBER: US/10/060,065

; PRIOR FILING DATE: 2002-01-29

; PRIOR APPLICATION NUMBER: PCT/JF00/05061

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/159,590

; PRIOR FILING DATE: 1999-10-18

; PRIOR APPLICATION NUMBER: US 60/183,322

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: JP 11-248036

; PRIOR FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: JP 2000-118776

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-158-23

Query Match 54.8%; Score 34; DB 7; Length 1338;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYI 7
DB 1165 DGKDYI 1170
|||||

RESULT 7

US-11-091-668-15
; Sequence 15, Application US/11091668
; Publication No. US20050262585A1
; GENERAL INFORMATION:
; APPLICANT: University of Nebraska
; APPLICANT: Mackenzie, Sally Ann
; APPLICANT: Vaghchhipawala, Zarir Erach
; TITLE OF INVENTION: Soybean FGAM Synthase Promoters Useful In Parasite Control
; FILE REFERENCE: 1231-221
; CURRENT APPLICATION NUMBER: US/11/091,668
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60556745
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-668-15

Query Match 53.2%; Score 33; DB 7; Length 60;
Best Local Similarity 50.0%; Pred. No. 3.8;
Matches 5; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 1 CDGKDYIVLP 10
DB 38 CDGRHLAVMP 47
|||||

RESULT 8

US-10-467-657-3702
; Sequence 3702, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3702
; LENGTH: 109
; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3702

Query Match 53.2%; Score 33; DB 6; Length 109;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 11
DB 13 NGADYVIPPI 22
:|||||

RESULT 9

US-10-467-657-3994
; Sequence 3994, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3994
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3994

Query Match 53.2%; Score 33; DB 6; Length 478;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 11
DB 21 DGRDNEVLVP 30
|||||

RESULT 10

US-11-147-238-2
; Sequence 2, Application US/11147238
; Publication No. US20050266534A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, Bettina, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE csta GENE
; FILE REFERENCE: 032301 WD 195
; CURRENT APPLICATION NUMBER: US/11/147,238
; CURRENT FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: US/09/935,799
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-147-238-2

Query Match 53.2%; Score 33; DB 7; Length 772;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYI 7
DB 119 DGKDYV 124
|||||

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RESULT 11
US-11-147-238-5
; Sequence 5, Application US/11147238
; Publication No. US20050266534A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, Bettina, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE csta GENE
; FILE REFERENCE: 032301 WD 195
; CURRENT APPLICATION NUMBER: US/11/147,238
; PRIOR FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: US/09/935,799
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-147-238-5

Query Match      53.2%; Score 33; DB 7; Length 772;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYI 7
Db      119 DGKDYV 124

RESULT 12
US-10-821-234-1219
; Sequence 1219, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1219
; LENGTH: 1133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1219

Query Match      53.2%; Score 33; DB 6; Length 1133;
Best Local Similarity 40.0%; Pred. No. 87;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLP 10
Db      435 CDTDDFVMVP 444

RESULT 13
US-10-467-657-7796
; Sequence 7796, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7796
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7796

Query Match      51.6%; Score 32; DB 6; Length 214;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVL 9
Db      24 EGEDYLVL 31
```

```
RESULT 14
US-11-000-463-279
; Sequence 279, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-279
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```
Query Match      51.6%; Score 32; DB 7; Length 224;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      214 CPGKRYDAIPL 224
```

```

RESULT 15
US-10-467-657-2238
; Sequence 2238, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2238
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2238

```

```

Query Match      51.6%; Score 32; DB 6; Length 234;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 GKDYIVLP 10
      |||:|
Db      179 GKDGWVLP 186

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Search completed: December 9, 2005, 10:39:53
Job time : 2.49057 secs

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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:24:10 ; Search time 45.8679 Seconds
(without alignments)
100.203 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	11	3	US-09-969-037-1
2	62	100.0	11	3	US-09-969-037-2
3	62	100.0	11	5	US-10-763-276-1
4	62	100.0	11	5	US-10-763-276-2
5	53	85.5	10	3	US-09-572-404B-4174
6	53	85.5	10	3	US-09-572-404B-4175
7	53	85.5	15	3	US-09-943-382-2
8	53	85.5	15	3	US-09-951-265-1
9	53	85.5	15	4	US-10-452-786-2
10	53	85.5	15	4	US-10-387-355-1
11	53	85.5	15	5	US-10-823-995-2
12	53	85.5	15	5	US-10-982-543-2
13	53	85.5	429	4	US-10-664-421-44
14	53	85.5	429	5	US-10-941-635-44
15	53	85.5	567	4	US-10-327-414-8
16	53	85.5	1306	5	US-10-741-600-1470
17	53	85.5	1354	4	US-10-262-538-30
18	53	85.5	1354	4	US-10-669-176-30
19	53	85.5	1356	3	US-09-969-037-7
20	53	85.5	1356	4	US-10-022-939-2
21	53	85.5	1356	4	US-10-100-405A-2
22	53	85.5	1356	4	US-10-327-414-6
23	53	85.5	1356	4	US-10-090-183-2
24	53	85.5	1356	4	US-10-165-193A-11
25	53	85.5	1356	4	US-10-394-322A-66
26	53	85.5	1356	4	US-10-440-464-129
27	53	85.5	1356	5	US-10-783-528-61

28	53	85.5	1356	5	US-10-872-198-115	Sequence 115, Appl
29	53	85.5	1356	5	US-10-763-276-7	Sequence 7, Appl
30	53	85.5	1356	5	US-10-741-600-1469	Sequence 1469, Ap
31	53	85.5	1356	5	US-10-741-600-1471	Sequence 1471, Ap
32	53	85.5	1356	5	US-10-926-806-10	Sequence 10, Appl
33	53	85.5	1356	5	US-10-824-982-2	Sequence 2, Appl
34	53	85.5	1356	6	US-11-021-951-115	Sequence 115, Appl
35	50	80.6	1345	4	US-10-090-183-6	Sequence 6, Appl
36	50	80.6	1367	3	US-09-919-408-6	Sequence 6, Appl
37	50	80.6	1367	3	US-09-766-678-2	Sequence 2, Appl
38	50	80.6	1367	3	US-09-872-136-6	Sequence 6, Appl
39	50	80.6	1367	4	US-10-165-193A-10	Sequence 10, Appl
40	50	80.6	1367	5	US-10-639-603-6	Sequence 6, Appl
41	50	80.6	1367	5	US-10-799-782-2	Sequence 2, Appl
42	50	80.6	1367	6	US-11-030-539-6	Sequence 6, Appl
43	47	75.8	136	4	US-10-425-115-363890	Sequence 363890,
44	41.5	66.9	426	5	US-10-471-758-3	Sequence 3, Appl
45	41	66.1	64	4	US-10-424-599-240544	Sequence 240544,

ALIGNMENTS

RESULT 1
US-09-969-037-1
; Sequence 1, Application US/09969037
; Publication No. US2003002247A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/969,037
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Phosphorylation
; LOCATION: 7
; OTHER INFORMATION: an antigen peptide for human KDR/Flk-1 phosphorylated at 1175-
; OTHER INFORMATION: tyrosine corresponding to its residue 1171-1180 and added cysteine
; OTHER INFORMATION: residue at the N-terminal
US-09-969-037-1

Query Match 100.0%; Score 62; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDGKDYIVLPI 11
|||||
Db 1 CDGKDYIVLPI 11

RESULT 2
US-09-969-037-2
; Sequence 2, Application US/09969037
; Publication No. US2003002247A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits biding of information transfer molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/969,037
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: JP 2000-303694

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: a peptide consisting of the same sequence as SEQ ID NO:1 without
US-09-969-037-2
;
Query Match      100.0%; Score 62; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      1 CDGKDYIVLPI 11

RESULT 3
US-10-763-276-1
; Sequence 1, Application US/10763276
; Publication No. US2005004003A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits binding of information
; TITLE OF INVENTION: transfer molecule for 1175-tyrosine phosphorylated KDR/Flk-1
; TITLE OF INVENTION: and usages of the same
; FILE REFERENCE: 249-199
; CURRENT APPLICATION NUMBER: US/10/763.276
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/969,037B
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Phosphorylation
; LOCATION: 7
; FEATURE:
; OTHER INFORMATION: an antigen peptide
US-10-763-276-1
;
Query Match      100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      1 CDGKDYIVLPI 11

RESULT 4
US-10-763-276-2
; Sequence 2, Application US/10763276
; Publication No. US2005004003A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Substance which inhibits binding of information
; TITLE OF INVENTION: transfer molecule for 1175-tyrosine phosphorylated KDR/Flk-1
; TITLE OF INVENTION: and usages of the same
; FILE REFERENCE: 249-199
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; CURRENT APPLICATION NUMBER: US/10/763.276
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/969,037B
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-303694
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/263,512
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: a peptide SEQ ID NO:1 without phosphorylation
US-10-763-276-2
;
Query Match      100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CDGKDYIVLPI 11
Db      1 CDGKDYIVLPI 11

RESULT 5
US-09-572-404B-4174
; Sequence 4174, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 4174
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in LCN1 OR VEGF at 1169-1178 and may interact wi
US-09-572-404B-4174
;
Query Match      85.5%; Score 53; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVLPI 11
Db      1 DGKDYIVLPI 10

RESULT 6
US-09-572-404B-4175
; Sequence 4175, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 4175
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
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; FEATURE:
; OTHER INFORMATION: sequence located in LCN1 OR VEGP at 1169-1178 and may interact w
; OTHER INFORMATION: Sequence 4174 in this patent.
US-09-572-404B-4175

Query Match      85.5%; Score 53; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1 DGKDYIVLPI 10

RESULT 7
US-09-943-382-2
; Sequence 2, Application US/09943382
; Publication No. US20020103230A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAPER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-943-382-2

Query Match      85.5%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 8
US-09-951-265-1
; Sequence 1, Application US/09951265
; Publication No. US20020107392A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAPER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/09/951,265
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

; FEATURE:
; OTHER INFORMATION: sequence located in LCN1 OR VEGP at 1169-1178 and may interact w
; OTHER INFORMATION: Sequence 4174 in this patent.
US-09-572-404B-4175

Query Match      85.5%; Score 53; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 1 DGKDYIVLPI 10

RESULT 7
US-09-943-382-2
; Sequence 2, Application US/09943382
; Publication No. US20020103230A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAPER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-943-382-2

Query Match      85.5%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 8
US-09-951-265-1
; Sequence 1, Application US/09951265
; Publication No. US20020107392A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAPER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/09/951,265
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

; FEATURE:
; OTHER INFORMATION: sequence located in LCN1 OR VEGP at 1169-1178 and may interact w
; OTHER INFORMATION: Sequence 4174 in this patent.
US-09-572-404B-4175

Query Match      85.5%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 8
US-10-387-355-1
; Sequence 1, Application US/10387355
; Publication No. US20040006101A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAPER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
```

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; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: C-term amidated
US-09-951-265-1

Query Match      85.5%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 9
US-10-452-786-2
; Sequence 2, Application US/10452786
; Publication No. US20040002518A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAPER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/10/452,786
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US/09/943,382
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-452-786-2

Query Match      85.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15

RESULT 10
US-10-387-355-1
; Sequence 1, Application US/10387355
; Publication No. US20040006101A1
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAPER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
```

; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/10/387,355
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/951,265
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-387-355-1

Query Match 85.5%; Score 53; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
| | | | |
Db 6 DGKDYIVLPI 15

RESULT 11

US-10-823-995-2
; Sequence 2, Application US/10823995
; Publication No. US20050137188A1

; GENERAL INFORMATION:
; APPLICANT: RENHOWER, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAFFER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/10/823,995
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/943,382
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-823-995-2

Query Match 85.5%; Score 53; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
| | | | |
Db 6 DGKDYIVLPI 15

RESULT 12

US-10-982-543-2
; Sequence 2, Application US/10982543

; Publication No. US20050209247A1
; GENERAL INFORMATION:
; APPLICANT: CAI, SHAOPEI
; APPLICANT: CHOU, JOYCE
; APPLICANT: HARWOOD, ERIC
; APPLICANT: MACHAJEWSKI, TIMOTHY
; APPLICANT: RYCKMAN, DAVID
; APPLICANT: SHANG, XIAO
; APPLICANT: ZHU, SHUGUANG
; TITLE OF INVENTION: PHARMACEUTICALLY ACCEPTABLE SALTS OF QUINOLINONE
; TITLE OF INVENTION: COMPOUNDS HAVING IMPROVED PHARMACEUTICAL PROPERTIES
; FILE REFERENCE: 072121-0440
; CURRENT APPLICATION NUMBER: US/10/982,543
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/546,017
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/526,425
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/526,426
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/517,915
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-982-543-2

Query Match 85.5%; Score 53; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
| | | | |
Db 6 DGKDYIVLPI 15

RESULT 13

US-10-664-421-44
; Sequence 44, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIVAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-44

Query Match 85.5%; Score 53; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 9, 2005, 10:39:35
Job time : 46.8679 secs

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QY      2 DGKDYIVLPI 11
Db      388 DGKDYIVLPI 397

RESULT 14
US-10-941-635-44
; Sequence 44, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-44

Query Match      85.5%; Score 53; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      388 DGKDYIVLPI 397

RESULT 15
US-10-327-414-8
; Sequence 8, Application US/10327414
; Publication No. US20030158083A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin G
; TITLE OF INVENTION: A Method of Effecting angiogenesis by Modulating the Function of
; TITLE OF INVENTION: Endothelia Phosphatase
; FILE REFERENCE: 8864M
; CURRENT APPLICATION NUMBER: US/10/327,414
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/355,125
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-414-8

Query Match      85.5%; Score 53; DB 4; Length 567;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      382 DGKDYIVLPI 391
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:23:55 ; Search time 13.6981 Seconds
(without alignments)
66.391 Million cell updates/sec

Title: US-10-763-276-1

Perfect score: 62

Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/H_COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/ECTUS_COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/RE_COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	53	85.5	15	2	US-09-943-382-2
3	53	85.5	15	2	US-10-452-786-2
4	53	85.5	15	2	US-10-387-355-1
5	53	85.5	1356	1	US-08-810-116-8
6	53	85.5	1356	1	US-07-930-548A-8
7	53	85.5	1356	2	US-09-098-707A-2
8	53	85.5	1356	2	US-09-483-539-2
9	53	85.5	1356	2	US-09-949-016-6198
10	53	85.5	1356	2	US-10-100-405A-2
11	53	85.5	1356	2	US-10-022-939-2
12	53	85.5	1456	2	US-09-949-016-9853
13	50	80.6	1367	1	US-07-813-593-4
14	50	80.6	1367	1	US-07-977-451-6
15	50	80.6	1367	1	US-07-946-507-4
16	50	80.6	1367	1	US-08-252-517-6
17	50	80.6	1367	1	US-07-306-397A-6
18	50	80.6	1367	1	US-08-601-891-6
19	50	80.6	1367	1	US-08-443-861-2
20	50	80.6	1367	1	US-09-021-324-6
21	50	80.6	1367	2	US-08-193-8298-2
22	50	80.6	1367	2	US-09-872-1368-6
23	50	80.6	1367	2	US-09-766-678-2
24	50	80.6	1367	2	US-09-919-408A-6
25	50	80.6	1367	4	PCT-US92-02750-8
26	50	80.6	1367	4	PCT-US92-05401-6
27	50	80.6	1367	4	PCT-US92-09893-6

28	40	64.5	115	2	US-08-936-165A-449	Sequence 449, App
29	40	64.5	294	2	US-09-902-540-16818	Sequence 16818, A
30	38	61.3	14	2	US-08-914-372C-16	Sequence 16, Appl
31	38	61.3	92	2	US-09-673-809-25	Sequence 25, Appl
32	38	61.3	92	2	US-09-673-809-104	Sequence 104, App
33	38	61.3	92	2	US-09-673-809-106	Sequence 106, App
34	38	61.3	156	2	US-09-513-999C-4289	Sequence 4289, Ap
35	38	61.3	181	2	US-09-013-077A-13	Sequence 13, Appl
36	38	61.3	182	1	US-08-127-954-135	Sequence 135, App
37	38	61.3	182	1	US-08-127-954-136	Sequence 136, App
38	38	61.3	182	1	US-08-127-954-137	Sequence 137, App
39	38	61.3	182	1	US-08-127-954-138	Sequence 138, App
40	38	61.3	182	1	US-08-127-954-139	Sequence 139, App
41	38	61.3	182	1	US-08-127-954-140	Sequence 140, App
42	38	61.3	182	1	US-08-127-954-141	Sequence 141, App
43	38	61.3	182	1	US-08-127-954-142	Sequence 142, App
44	38	61.3	182	1	US-08-127-954-143	Sequence 143, App
45	38	61.3	182	1	US-08-127-954-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-09-951-265-1
; Sequence 1, Application US/09951265
; Patent No. 6605617
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAFER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/09/951,265
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-951-265-1

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
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Db 6 DGKDYIVLPI 15

RESULT 2
US-09-943-382-2
; Sequence 2, Application US/09943382
; Patent No. 6756383
; GENERAL INFORMATION:
; APPLICANT: RENHOWE, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SCHAFER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN

; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-09-943-382-2

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15
|||||

RESULT 3
US-10-452-786-2
; Sequence 2, Application US/10452786
; Patent No. 6759417
; GENERAL INFORMATION:
; APPLICANT: RENHOM, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAFER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/10/452,786
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US/09/943,382
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-452-786-2

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15
|||||

RESULT 4
US-10-387-355-1
; Sequence 1, Application US/10387355
; Patent No. 6762194

; GENERAL INFORMATION:
; APPLICANT: RENHOM, PAUL A.
; APPLICANT: PECCHI, SABINA
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAFER, CYNTHIA M.
; APPLICANT: TAYLOR, CLARKE
; APPLICANT: MCCREA, WILLIAM R. JR
; APPLICANT: MCBRIDE, CHRISTOPHER
; APPLICANT: JAZAN, ELISA
; TITLE OF INVENTION: QUINOLINONE DERIVATIVES
; FILE REFERENCE: 072121/0141
; CURRENT APPLICATION NUMBER: US/10/387,355
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/951,265
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/232,159
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-387-355-1

Query Match 85.5%; Score 53; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 6 DGKDYIVLPI 15
|||||

RESULT 5
US-08-810-116-8
; Sequence 8, Application US/08810116
; Patent No. 5766860
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5766860a1 Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/810,116
; APPLICATION NUMBER: 25-FEB-1997
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/930,548
; FILING DATE: 23-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,298-01
; TELECOMMUNICATION INFORMATION:


```
;
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-116-8

Query Match      85.5%; Score 53; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 6
US-07-930-548A-8
; Sequence 8, Application US/07930548A
; Patent No. 5861301
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5861301e1 Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07930,548A
; FILING DATE: 23-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,298-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-930-548A-8

Query Match      85.5%; Score 53; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 7
US-09-098-707A-2
; Sequence 2, Application US/09098707A
; Patent No. 6204011
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew J.
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,707A
; FILING DATE: 17-Jun-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19963PV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732/594-3905
; TELEFAX: 732/594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-098-707A-2

Query Match      85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 8
US-09-483-539-2
; Sequence 2, Application US/09483539
; Patent No. 6359115
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew J.
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,539
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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19963pv
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732/594-3905
; TELEFAX: 732/594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-483-539-2
    Query Match      85.5%; Score 53; DB 2; Length 1356;
    Best Local Similarity 100.0%; Pred. No. 0.42;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 9
US-09-949-016-6198
; Sequence 6198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6198
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6198

    Query Match      85.5%; Score 53; DB 2; Length 1356;
    Best Local Similarity 100.0%; Pred. No. 0.42;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 10
US-10-100-405A-2
; Sequence 2, Application US/10100405A
; Patent No. 6811367
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDC
; CURRENT APPLICATION NUMBER: US/10/100,405A
; CURRENT FILING DATE: 2002-08-13
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; PRIOR APPLICATION NUMBER: 10/022,939
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-100-405A-2

    Query Match      85.5%; Score 53; DB 2; Length 1356;
    Best Local Similarity 100.0%; Pred. No. 0.42;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 11
US-10-022-939-2
; Sequence 2, Application US/10022939
; Patent No. 6841382
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi
; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Human
US-10-022-939-2

    Query Match      85.5%; Score 53; DB 2; Length 1356;
    Best Local Similarity 100.0%; Pred. No. 0.42;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DGKDYIVLPI 11
Db      1171 DGKDYIVLPI 1180

RESULT 12
US-09-949-016-9853
; Sequence 9853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: 60/241,755
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;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 9853
;; LENGTH: 1456
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-9853

Query Match 85.5%; Score 53; DB 2; Length 1456;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
|||||
Db 1271 DGKDYIVLPI 1280

RESULT 13
US-07-813-593-4
; Sequence 4, Application US/07813593
; Patent No. 5185438
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,593
; FILING DATE: 19920415
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-813-593-4

Query Match 80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. No. 1.5;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DGKDYIVLPI 11
|||||
Db 1169 DGKDYIVLPM 1178
RESULT 14
US-07-977-451-6
; Sequence 6, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-977-451-6

Query Match 80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. NO. 1.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1169 DGKDYIVLPM 1178

RESULT 15

US-07-946-507-4
; Sequence 4, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946.507
; FILING DATE: 19920917
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/813.593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/793.065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/728.913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/679.666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1367 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-946-507-4

Query Match 80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. NO. 1.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 1169 DGKDYIVLPM 1178

Search completed: December 9, 2005, 10:35:48
Job time : 13.6981 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:19:24 ; Search time 57.4906 Seconds
(without alignments)
84.069 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	11	5	Aau79424 Human KDR
2	53	85.5	10	4	Aag97980 Human com
3	53	85.5	10	4	Aag97979 Human com
4	53	85.5	429	9	Ady85472 Catalytic
5	53	85.5	1306	8	Adq39807 Human myo
6	53	85.5	1354	9	Adz00446 VEGFR-2.
7	53	85.5	1355	2	Aaw80997 Human rec
8	53	85.5	1356	2	Aar26999 Novel typ
9	53	85.5	1356	2	Aaw59275 Human KDR
10	53	85.5	1356	4	Aab62475 Human VEG
11	53	85.5	1356	4	Aay97783 Human KDR
12	53	85.5	1356	4	Aay97576 Human Flk
13	53	85.5	1356	5	Aau79427 Human Kin
14	53	85.5	1356	5	Aau79429 Human Kin
15	53	85.5	1356	5	Aau79426 Human Kin
16	53	85.5	1356	6	Abz40196 Human vas
17	53	85.5	1356	7	Add08954 Human VEG
18	53	85.5	1356	7	Abm79007 Human VEG
19	53	85.5	1356	7	Adf45097 Human kin
20	53	85.5	1356	7	Abu64302 Human KDR
21	53	85.5	1356	8	Adh17130 Human vas
22	53	85.5	1356	8	Adg70543 Human KDR
23	53	85.5	1356	8	Adq39806 Human myo
24	53	85.5	1356	8	Adq39808 Human myo

25	53	85.5	1356	8	ADR46648	Adr46648	Cancer-as
26	53	85.5	1356	8	ADT92353	Adt92353	Human vas
27	53	85.5	1356	9	ADY90285	Ady90285	Protease-
28	53	85.5	1356	9	ADY59385	Ady59385	Human VEG
29	53	85.5	1356	9	ADZ26561	Adz26561	Human VEG
30	50	80.6	558	8	ADR32352	Adr32352	Rat recep
31	50	80.6	820	8	ADR32354	Adr32354	GST-rat K
32	50	80.6	1343	8	ADR32351	Adr32351	Rat recep
33	50	80.6	1343	8	ADR32338	Adr32338	Rat optim
34	50	80.6	1345	7	ABM79009	Abm79009	Murine Fl
35	50	80.6	1367	2	AAR28041	Aar28041	flk-1, 3/
36	50	80.6	1367	2	AAR31377	Aar31377	Human flk
37	50	80.6	1367	2	AAR37504	Aar37504	Murine fl
38	50	80.6	1367	2	AAR44996	Aar44996	Murine fl
39	50	80.6	1367	2	AAR54046	Aar54046	Sequence
40	50	80.6	1367	2	AAR67537	Aar67537	Mouse flk
41	50	80.6	1367	2	AAR67817	Aar67817	Flk1 rece
42	50	80.6	1367	2	AAR97420	Aar97420	Murine fo
43	50	80.6	1367	2	AAW19875	Aaw19875	Murine fl
44	50	80.6	1367	2	ADP90725	Adp90725	Mouse foe
45	50	80.6	1367	2	AAV08618	Aay08618	Murine fl

ALIGNMENTS

RESULT 1
AAU79424
ID AAU79424 standard; peptide; 11 AA.
XX
AC AAU79424;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human KDR/FLK-1 phosphorylated antigenic peptide.
XX

KW Human; KDR; kinase insert domain-containing receptor; FLK-1;
KW fetal liver kinase-1; cytotostatic; antidiabetic; antirheumatic;
KW antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis;
KW immunogen.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1 /note= "Non-human added C terminal Cys"
FT Modified-site 6 /label= OTHER
FT /note= "Tyr is optionally phosphorylated".

WO200229090-A1.

11-APR-2002.

02-OCT-2001; 2001WO-JP008684.

03-OCT-2000; 2000JP-00303694.

(KYOW) KYOWA HAKKO KOGYO KK.

(SHIBU) SHIBUYA M.

Shibuya M, Takahashi T, Furuya A, Shitara K;

WPI; 2002-352237/38.

Screening substances inhibiting the binding of signal-transducing molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as cell proliferation inhibitors and angiogenesis inhibitors for treatment of e.g., tumor.

Example 1; Page 63; 81pp; Japanese.

XX The invention relates to inhibiting the signal transduction of KDR/Flk-1
 CC (kinase insert domain-containing receptor/fetal liver kinase-1) is by
 CC using a substance inhibiting the binding of a signal-transducing molecule
 CC to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
 CC included are methods of detecting/inhibiting/screening for cell
 CC proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
 CC phosphorylation at tyrosine at the 1175-position using the binding
 CC inhibitors, compounds obtained by the screening methods, drugs containing
 CC the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-
 CC -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
 CC monoclonal antibody or its fragment, a recombinant vector containing the
 CC DNA and a transformant obtained by transferring the recombinant vector
 CC into a host cell. The method is useful for screening substances
 CC inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
 CC phosphorylated at tyrosine at 1175-position, as cell proliferation
 CC inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
 CC diabetic omentopathy and chronic rheumatoid arthritis. A method for
 CC detecting angiogenesis is also provided. The present sequence is a
 CC peptide based on residues 1171-1180 of KDR/FLK-1 used to generate
 CC antibodies against the 1175-position phosphorylated KDR/FLK-1
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDGKDYIVLPI 11
 |||||
 Db 1 CDGKDYIVLPI 11

RESULT 2

AAG97980
 ID AAG97980 standard; peptide; 10 AA.

XX AC AAG97980;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 4175.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB004776.

XX PR 13-DEC-1999; 99GB-00029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX PX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX PS Example 6; Page 631; 646pp; English.

XX The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided

CC in the specification
 XX Sequence 10 AA;

Query Match 85.5%; Score 53; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
 |||||
 Db 1 DGKDYIVLPI 10

RESULT 3

AAG97979
 ID AAG97979 standard; peptide; 10 AA.

XX AC AAG97979;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 4174.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB004776.

XX PR 13-DEC-1999; 99GB-00029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX PX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX PS Example 6; Page 631; 646pp; English.

XX The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification

XX SQ Sequence 10 AA;

Query Match 85.5%; Score 53; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
 |||||
 Db 1 DGKDYIVLPI 10

RESULT 4

ADY85472
 ID ADY85472 standard; protein; 429 AA.

XX AC ADY85472;

XX DT 16-JUN-2005 (first entry)

XX Catalytic domain of PIM kinase-like protein VEGFR.
DE Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
XX neoplasm; inflammation; antiinflammatory.
KW Unidentified.
OS WO2005028624-A2.
XX 31-MAR-2005.
PD 15-SEP-2004; 2004WO-US030360.
XX 15-SEP-2003; 2003US-0503277P.
XX (PLEX-) PLEXIKON INC.
XX Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX WPI; 2005-273155/28.
XX New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX Disclosure; Page 170-174; 236pp; English.
XX The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII)), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the component or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group), and developing a ligand for a kinase
CC comprising conserved residues matching at least one of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gak3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease

CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX SQ Sequence 429 AA;
Query Match 85.5%; Score 53; DB 9; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGKDYIVLPI 11
| | | | | | | | | |
DB 388 DGKDYIVLPI 397
RESULT 5
ADQ39807
ID ADQ39807 standard; protein; 1306 AA.
XX
AC ADQ39807;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1470.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
cardiant; gene therapy; human.
OS Homo sapiens.
XX WO2004058052-A2.
XX 15-JUL-2004.
PD 22-DEC-2003; 2003WO-US040978.
PF 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX (APPL-) APPLERA CORP.
PA Cargill M, Devlin JJ, Iakoubova O;
XX WPI; 2004-533949/51.
XX N-PSDB; ADQ38979.
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX Claim 10; SEQ ID NO 1470; 145pp; English.
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification, an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction.
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1306 AA;
 QY Query Match 85.5%; Score 53; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 DGKDYIVLPI 11
 1121 DGKDYIVLPI 1130

RESULT 6
 ADZ00446
 ID ADZ00446 standard; protein; 1354 AA.

AC ADZ00446;

XX 16-JUN-2005 (first entry)

DE VEGFR-2.

VEGF-C agonist; VEGF-D agonist; Nootropic; Neuroprotective;
 Antiparkinsonian; Anticonvulsant; CNS-Gen.; Antiinflammatory; Anti-HIV;
 Virucide; Vasotropic; vascular endothelial growth factor C; VEGF-C;
 vascular endothelial growth factor D; VEGF-D; recruitment; proliferation;
 differentiation; migration; survival; neural cell; precursor; VEGFR-3;
 neuropilin-2; VEGF-C deltaC156; heparin-binding VEGF-C;
 neurotherapeutic; interferon gamma; nerve growth factor;
 epidermal growth factor; EGF; basic fibroblast growth factor; bFGF;
 neurogenin; brain derived neurotrophic factor; BDNF; thyroid hormone;
 bone morphogenic protein; BMP; leukemia inhibitory factor; LIF;
 sonic hedgehog; glial cell line-derived neurotrophic factor; GDNF;
 vascular endothelial growth factor; VEGF; interleukin; interferon;
 stem cell factor; SCF; activin; inhibin; chemokine; retinoic acid;
 ciliary neurotrophic factor; CNTF; tacrine; Cognex; donepezil; Aricept;
 rivastigmine; Exelon; galantamine; Reminyl; cholinesterase inhibitor;
 anti-inflammatory; anti-cholinergic; dopamine agonist;
 catechol-0-methyl-transferase; COMT; amantadine; Symmetrel; Sinemet;
 Selegiline; carbidopa; ropinirole; Requip; coenzyme Q10; Pramipexole;
 Mirapex; levodopa; L-dopa; Alzhemers disease; Parkinsons disease;
 Huntingtons disease; motor neuron disease;
 Amylotrophic Lateral Sclerosis; ALS; dementia; cerebral palsy;
 demyelination; multiple sclerosis; phenylketonuria;
 periventricular leukomalacia; PVL; HIV-1 encephalitis; HIVE;
 Guillian Barre Syndrome; GBS;
 acute inflammatory demyelinating polynuropathy; AIDP;
 acute motor axonal neuropathy; AMAN;
 acute motor sensory axonal neuropathy; AMSAN; Fisher syndrome;
 acute pandysautonomia;
 chronic inflammatory demyelinating polyradiculoneuropathy; CIDP;
 multifocal acquired demyelinating sensory and motor neuropathy; MADSAM;
 Lewis-Sumner syndrome;
 distal acquired demyelinating symmetric neuropathy; DADS; neural trauma;
 neural injury; stroke; spinal cord injury; post-operative injury;
 brain ischemia; neuroblastoma; neural tumor.

OS Homo sapiens.

XX WO2005030240-A2.

XX 07-APR-2005.
 PD 23-SEP-2004; 2004WO-US031318.
 PF 23-SEP-2003; 2003US-00669176.
 PR 23-SEP-2003; 2003US-0505607P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX Alitalo K, Karkkainen M, Haiko P, Sainio K, Wartiovaara K;
 PI Thomas JL, Eichmann A;
 XX WPI; 2005-273287/28.
 DR N-PSDB; ADZ00445.
 DR GENBANK; L04947.
 XX Use of a vascular endothelial growth factor-C or -D product in
 PT medicaments for promoting growth and differentiation of neural stem cells
 PT for neurodegenerative disorders such as Alzheimer's and Parkinson's
 PT disease.
 XX Disclosure; SEQ ID NO 28; 263pp; English.
 PS This sequence represents VEGFR-2. The method of the invention uses a
 XX vascular endothelial growth factor-C (VEGF-C) product or a vascular
 CC endothelial growth factor D (VEGF-D) product in the manufacture of a
 CC medicament to promote recruitment, proliferation, differentiation,
 CC migration or survival of neural cells or neural precursor cells. The
 CC method of the invention comprises identifying a mammalian subject in need
 CC of treatment to promote recruitment, proliferation, differentiation,
 CC migration, or survival of neural cells or neural precursor cells, and
 CC administering to the subject a composition comprising a VEGF-C or VEGF-D
 CC product. The product is a VEGF-C product comprising a purified mammalian
 CC prepro-VEGF-C polypeptide or its fragment that binds VEGFR-3 or
 CC neuropilin-2, a VEGF-C deltaC156 polypeptide, or a chimeric heparin-
 CC binding VEGF-C polypeptide. The method also comprises administering to
 CC the mammalian subject a neurotherapeutic agent, and including in the
 CC medicament a neurotherapeutic agent. The neurotherapeutic agent comprises
 CC a neural growth factor and/or a polynucleotide encoding a neural growth
 CC factor selected from interferon gamma, nerve growth factor, epidermal
 CC growth factor (EGF), basic fibroblast growth factor (bFGF), neurogenin,
 CC brain derived neurotrophic factor (BDNF), thyroid hormone, bone
 CC morphogenic proteins (BMPs), leukemia inhibitory factor (LIF), sonic
 CC hedgehog, glial cell line-derived neurotrophic factor (GDNF), vascular
 CC endothelial growth factor (VEGF), interleukins, interferons, stem cell
 CC factor (SCF), activins, inhibins, chemokines, retinoic acid and ciliary
 CC neurotrophic factor (CNTF). The neurotherapeutic agent is also tacrine
 CC (Cognex), donepezil (Aricept), rivastigmine (Exelon), galantamine
 CC (Reminyl), cholinesterase inhibitors or anti-inflammatory drugs, and/or
 CC is anti-cholinergics, dopamine agonists, catechol-0-methyl-transferases
 CC (COMTs), amantadine (Symmetrel), Sinemet (RTM), Selegiline, carbidopa,
 CC ropinirole (Requip), coenzyme Q10, Pramipexole (Mirapex) and levodopa (L-
 CC dopa). The medicament of the invention is for the treatment of a disease
 CC or condition characterized by aberrant growth of neuronal cells, neuronal
 CC scarring, or neural degeneration, or for treatment of neural degeneration
 CC caused by a neurodegenerative disorder selected from the group consisting
 CC of Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC motor neuron disease, Amylotrophic Lateral Sclerosis (ALS), dementia and
 CC cerebral palsy, and for treatment of a disease or condition with aberrant
 CC growth of oligodendrocyte or oligodendrocyte precursor cells, where the
 CC condition has demyelination in the nervous system. The medicament is also
 CC for the treatment of multiple sclerosis, phenylketonuria, periventricular
 CC leukomalacia (PVL), HIV-1 encephalitis (HIVE), Guillian Barre Syndrome
 CC (GBS), acute inflammatory demyelinating polynuropathy (AIDP), acute
 CC motor axonal neuropathy (AMAN), acute motor sensory axonal neuropathy
 CC (AMSAN), Fisher syndrome, acute pandysautonomia, and Krabbe's disease.
 CC The medicament can also be used for the treatment of chronic inflammatory
 CC demyelinating polyradiculoneuropathy (CIDP), such as multifocal acquired
 CC demyelinating sensory and motor neuropathy (MADSAM, also know as Lewis-
 CC Sumner syndrome) and distal acquired demyelinating symmetric neuropathy

CC (DADS), and for the treatment of neural trauma or neural injury, where
 CC the neural trauma is a stroke-related injury, spinal cord injury, post-
 CC operative injury or brain ischemia. The VEGF-C inhibitor is useful in the
 CC manufacture of a medicament for the treatment of a neuroblastoma or
 CC neural tumor. The methods and compositions of the present invention are
 CC also useful for cellular and molecular biology and medicine, in
 CC particular for the vascularization and angiogenesis and the interactions
 CC of the vascular system with the nervous system.

XX Sequence 1354 AA;

Query Match 85.5%; Score 53; DB 9; Length 1354;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
 |||||
 DB 1169 DGKDYIVLPI 1178

RESULT 7

ID AAW80997 standard; protein; 1355 AA.

XX AAW80997;

DT 12-APR-1999 (first entry)

XX Human receptor tyrosine kinase KDR.

XX KDR; receptor tyrosine kinase; human; signal transduction; mitogen;
 KW neangiogenesis; angiogenesis; diabetic retinopathy; breast cancer;
 KW brain cancer; inflammation; rheumatoid arthritis; psoriasis;
 KW contact dermatitis; hypersensitivity; antagonist; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 780..1386
 FT /note= "intracellular domain, from about amino acid 780-
 FT 795 to about amino acid 1175-1386"

PN W09858053-A1.

XX 23-DEC-1998.

XX 17-JUN-1998; 98WO-US012569.

XX 18-JUN-1997; 97US-0050962P.

XX (MERI) MERCK & CO INC.

XX Kendall RL, Thomas KA, Mao X, Tebben A;

PI WPI; 1999-095333/08.

DR N-PSDB; AAV99829.

XX Human receptor tyrosine kinase protein, KDR - useful e.g. to screen for
 FT antagonists useful to treat diseases involving neangiogenesis e.g.
 FT diabetic retinal vascularization, cancers.

XX Claim 2; Fig 2; 69pp; English.

XX This is the amino acid sequence of a novel receptor tyrosine kinase,
 CC termed KDR, that is expressed on human endothelial cells. KDR is
 CC activated by vascular endothelial growth factor and mediates a mitogenic
 CC signal. It is implicated in clinical neangiogenesis. The amino acid
 CC sequence was deduced from an isolated KDR cDNA (see AAV99829). The
 CC predicted sequence has differences from the previously published KDR
 CC sequence at positions 498 (Ala to Glu), 772 (Thr to Ala), 787 (Gly to
 CC Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347 (Thr to Ser), producing
 CC a protein predicted by computer modeling to have higher activity and
 CC functionality. The invention also relates to recombinant vectors and

CC recombinant hosts which contain a DNA fragment encoding human KDR, a DNA
 CC fragment encoding the intracellular portion of KDR with or without a
 CC membrane anchor sequence, purified forms of associated human KDR, and
 CC human mutant forms of KDR. KDR, fusion proteins or fragments can be used
 CC in assays to identify antagonists and agonists of human KDR (claimed).
 CC Antagonists of KDR useful for treating diseases involving neangiogenesis
 CC e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.)
 CC and forms of inflammation e.g. rheumatoid arthritis, psoriasis, contact
 CC dermatitis and hypersensitivity reactions. The protein is also useful for
 CC produce antibodies that can be used to measure human KDR levels and/or
 CC activity

XX Sequence 1355 AA;

Query Match 85.5%; Score 53; DB 2; Length 1355;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
 |||||
 DB 1170 DGKDYIVLPI 1179

RESULT 8

AAR26999

ID AAR26999 standard; protein; 1356 AA.

XX AAR26999;

XX 23-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX Novel type III RTK encode by the KDR gene.

XX Receptor tyrosine kinase; vascular endothelial cell growth factors;
 KW cancer; tumour; diagnosing; monitoring.

XX Homo sapiens.

XX Unidentified.

XX Key Location/Qualifiers

FT Domain 1..763
 FT /note= "putative extracellular region - contains 21
 FT cysteine residues"
 FT 46
 FT Modified-site /note= "potential N linked glycosylation site"
 FT 66
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 96
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 143
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 158
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 245
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 318
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 374
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 395
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 511
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 523
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 580
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 613
 FT Modified-site /note= "potential N-linked glycosylation site"
 FT 631
 FT Modified-site /note= "potential N-linked glycosylation site"

PS Claim 1; Fig 7A-M; Slipp; English.

CC This sequence represents a novel human growth factor receptor, kinase

CC insert domain containing receptor or KDR. This receptor is capable of

CC binding to the vascular endothelial cell growth factor, VEGF and is used

CC in a screening assay which identifies compounds that inhibit VEGF action

CC on KDR. Such compounds which inhibit binding of VEGF to the KDR may

CC inhibit angiogenesis and thus be useful for treating cancer

XX

XX Sequence 1356 AA;

SQ

Query Match 85.5%; Score 53; DB 2; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

DB 1171 DGKDYIVLPI 1180

RESULT 10

AA62475

ID AAB62475 standard; protein; 1356 AA.

XX AC AAB62475;

XX

XX 09-JUL-2001 (first entry)

DT

XX Human VEGFR-2 receptor protein.

DE

XX Receptor protein; vascular endothelial growth factor receptor-2; VEGFR-2;

KW neuropilin-1; NP-1; co-receptor; human; angiogenic.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH Domain 1..760

FT /note= "extracellular domain"

FT Domain 124..320

FT /note= "Ig domain"

XX

XX WO200131346-A2.

XX

XX 03-MAY-2001.

PD

XX 26-OCT-2000; 2000WO-US029579.

PF

XX 28-OCT-1999; 99US-0162367P.

XX

XX (PROC) PROCTER & GAMBLE CO.

PA

XX Rosenbaum JS, Whitaker GB, Limberg BJ;

PI

XX WPI; 2001-308686/32.

DR

XX N-PSDB; AAF83308.

DR

XX Determining compounds which bind to a complex comprising vascular

FT endothelial growth factor receptor-2 and Neuropilin-1 to provide superior

PT pro- and anti-angiogenic agents.

PT

XX Claim 7; Page 32-39; 82pp; English.

PS

XX The invention relates to determining whether a compound is capable of

CC binding to a receptor protein complex comprising a vascular endothelial

CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1

CC (NP-1) receptor protein. One method comprises introducing a sample

CC comprising the compound to the receptor protein and allowing the compound

CC to bind to the complex. Signaling through VEGFR-2 is enhanced in the

CC presence of the NP-1 co-receptor. The methods of the invention can be

CC used for identifying novel pro- and anti-angiogenic compounds. The

CC present sequence represents the human VEGFR-2 receptor protein

XX

XX Sequence 1356 AA;

SQ

Query Match 85.5%; Score 53; DB 4; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

DB 1171 DGKDYIVLPI 1180

RESULT 11

AA97783

ID AAY97783 standard; protein; 1356 AA.

XX AC AAY97783;

XX

XX 22-AUG-2001 (first entry)

DT

XX Human KDR/Flk-1 protein.

DE

XX Immunoglobulin-like domain; Ig-like domain; retinal neovascularisation;

KW vascular endothelial growth factor receptor; VEGF receptor; inflammation;

KW psoriasis; rheumatoid arthritis; haemangioma; leiomyoma; angiofibroma;

KW diabetic retinopathy; endometriosis; macular degeneration; cancer;

KW dimerisation inhibitor; therapy; KDR/Flk-1; human.

XX

XX Homo sapiens.

OS

XX WO200142284-A2.

PN

XX 14-JUN-2001.

PD

XX 07-DEC-2000; 2000WO-GB004693.

PF

XX 07-DEC-1999; 99GB-00028950.

PR

XX (METR-) METRIS THERAPEUTICS LTD.

PA

XX Pappa H;

PI

XX WPI; 2001-381631/40.

DR

XX Novel proteins that prevent dimerization of vascular endothelial growth

PT factor receptors and for treating diseases in which the receptor plays a

PT role e.g. inflammation, cancer, diabetic retinopathy, psoriasis.

PT

XX Claim 11; Fig 3; 83pp; English.

PS

XX This sequence represents the human KDR/Flk-1 protein. The invention

CC relates to a protein comprising the amino acid sequence of the fourth

CC immunoglobulin (Ig)-like domain of a vascular endothelial growth factor

CC (VEGF) receptor or a variant of the protein that retains the ability to

CC bind to a VEGF receptor. The protein, its functional equivalent and DNA

CC encoding it are useful for treating a disorder whose pathology is

CC dependent upon a VEGF family-mediated pathway, including inflammation,

CC psoriasis, rheumatoid arthritis, haemangiomas, leiomyomas, diabetic

CC retinopathy, angiofibromas, endometriosis, macular degeneration, retinal

CC neovascularisation or cancer. The protein or its functional equivalents

CC are also useful for inhibiting the dimerisation of a VEGF receptor

XX

XX Sequence 1356 AA;

SQ

Query Match 85.5%; Score 53; DB 4; Length 1356;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

DB 1171 DGKDYIVLPI 1180

RESULT 12

AA97576

```

ID  AA97576 standard; protein; 1356 AA.
XX
AC  AA97576;
XX
DT  05-APR-2001 (first entry)
XX
DE  Human Flk-1 transmembrane and extracellular domains.
XX
KW  Human; angiogenic protein; wound healing; vascular tissue repair;
KW  peripheral arterial disease; critical limb ischaemia; coronary disease;
KW  angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
KW  rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
KW  infectious disease; neurodegeneration; Flk-1.
XX
OS  Homo sapiens.
XX
PN  WO200075163-A1.
XX
PD  14-DEC-2000.
XX
PF  01-JUN-2000; 2000WO-US014925.
XX
PR  03-JUN-1999; 99US-0137796P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Rosen CA, Ruben SM, Hu J, Cao L;
XX  WPI; 2001-071057/08.
XX
PT  New nucleic acid encoding angiogenic proteins, useful e.g. for promoting
PT  healing of wounds and treating peripheral arterial disease, critical limb
PT  ischemia or coronary disease.
XX
PS  Example 48; Page 236-240; 244pp; English.
XX
CC  This sequence is a human Flk-1 fragment, and was used in the isolation of
CC  an angiogenic protein of the invention. The angiogenic proteins and the
CC  DNA sequences encoding them, are used to prevent, treat or ameliorate
CC  disease and to detect diseases, or susceptibility, by detecting mutations
CC  or the presence or amount of angiogenic protein expression. Particularly
CC  they are used to stimulate wound healing, growth of damaged bone and
CC  tissue, and for repair of vascular tissue, especially peripheral arterial
CC  disease, critical limb ischaemia or coronary disease. Antagonists of the
CC  sequences are used to inhibit angiogenesis in tumours and to treat
CC  inflammation (where associated with increased vascular permeability),
CC  diabetic retinopathy, rheumatoid arthritis or psoriasis. Agonists are
CC  also useful for stimulating (lymph)angiogenesis. The proteins are also
CC  used to identify specific binding agents (potential therapeutic agents)
CC  and to raise antibodies. The antibodies are useful as therapeutic
CC  (ant)agonists; for detection, purification and targeting of proteins for
CC  in vivo or in vitro diagnosis (including imaging) or for therapy
CC  (including when linked to e.g. a label or cytotoxin); and for
CC  immunotyping of cells, e.g. for detecting minimal residual disease or
CC  haematopoietic progenitor/stem cells. It is also contemplated that the
CC  sequences might be useful for treating a very wide range of other
CC  disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases
CC  (viral, bacterial, fungal or parasitic); neurodegeneration, also as
CC  chemotactic agents or for stimulating regeneration of the nervous system
CC  etc
XX
SQ  Sequence 1356 AA;

Query Match      85.5%; Score 53; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 DGKDYIVLPI 11
Db  1171 DGKDYIVLPI 1180
      |||||
RESULT 13

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AAU79427
ID  AAU79427 standard; protein; 1356 AA.
XX
AC  AAU79427;
XX
DT  02-JUL-2002 (first entry)
XX
DE  Human Kinase insert domain-containing receptor mutant Y801F.
XX
KW  Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
KW  fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic; mutein;
KW  antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW  angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX
OS  Homo sapiens.
XX
PN  WO200229090-A1.
XX
PD  11-APR-2002.
XX
PF  02-OCT-2001; 2001WO-JP008684.
XX
PR  03-OCT-2000; 2000JP-00303694.
XX
PA  (KYOW ) KYOWA HAKKO KOGYO KK.
XX  (SHIB/) SHIBUYA M.
XX
PI  Shibuya M, Takahashi T, Furuya A, Shitara K;
XX  WPI; 2002-352237/38.
XX
PT  Screening substances inhibiting the binding of signal-transducing
PT  molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT  cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT  of e.g. tumor.
XX
PS  Example 8; Page; 81pp; Japanese.
XX
CC  The invention relates to inhibiting the signal transduction of KDR/Flk-1
CC  (kinase insert domain-containing receptor/fetal liver kinase-1) is by
CC  using a substance inhibiting the binding of a signal-transducing molecule
CC  to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
CC  included are methods of detecting/inhibiting/screening for cell
CC  proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
CC  phosphorylation at tyrosine at the 1175-position using the binding
CC  inhibitors, compounds obtained by the screening methods, drugs containing
CC  the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk
CC  -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
CC  monoclonal antibody or its fragment, a recombinant vector containing the
CC  DNA and a transformant obtained by transferring the recombinant vector
CC  into a host cell. The method is useful for screening substances
CC  inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
CC  phosphorylated at tyrosine at 1175-position, as cell proliferation
CC  inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
CC  diabetic omentopathy and chronic rheumatoid arthritis. A method for
CC  detecting angiogenesis is also provided. The present sequence is the
CC  Human KDR/FLK-1 mutant where Tyr at 801 is replaced by Phe. Note: The
CC  present sequence is not shown in the specification but was created by the
CC  indexer using the KDR/FLK-1 sequence appearing as AAU74926 and the
CC  information in example 8
XX
SQ  Sequence 1356 AA;

Query Match      85.5%; Score 53; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 DGKDYIVLPI 11

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Db      1171 DGKDYIVLPI 1180
|||||
AAU79429 standard; protein; 1356 AA.
AC      AAU79429;
XX
XX
XX      02-JUL-2002 (first entry)
DE      Human Kinase insert domain-containing receptor mutant Y1214F.
XX
XX      Human; KDR; kinase insert domain-containing; receptor; FLK-1; mutant;
KW      fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic; muten;
KW      antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW      angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      Misc-difference 1214
FT      /note= "Wild-type Tyr substituted by Phe"
XX
XX      WO200229090-A1.
PN
XX
XX      11-APR-2002.
PD
XX
XX      02-OCT-2001; 2001WO-JP008684.
PF
XX
XX      03-OCT-2000; 2000JP-00303694.
PR
XX
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
PA      (SHIB/) SHIBUYA M.
XX
XX      Shibuya M, Takahashi T, Furuya A, Shitara K;
PI      WPI; 2002-352237/38.
XX
XX      Screening substances inhibiting the binding of signal-transducing
PT      molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT      cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT      of e.g. tumor.
XX
XX      Example 8; Page; 81pp; Japanese.
XX
XX      The invention relates to inhibiting the signal transduction of KDR/Flk-1
XX      (kinase insert domain-containing receptor/fetal liver kinase-1) is by
XX      using a substance inhibiting the binding of a signal-transducing molecule
XX      to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
XX      included are methods of detecting/inhibiting/screening for cell
XX      proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
XX      phosphorylation at tyrosine at the 1175-position using the binding
XX      inhibitors, compounds obtained by the screening methods, drugs containing
XX      the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-
XX      -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
XX      monoclonal antibody or its fragment, a recombinant vector containing the
XX      DNA and a transformant obtained by transferring the recombinant vector
XX      into a host cell. The method is useful for screening substances
XX      inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
XX      phosphorylated at tyrosine at 1175-position, as cell proliferation
XX      inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
XX      diabetic omentopathy and chronic rheumatoid arthritis. A method for
XX      detecting angiogenesis is also provided. The present sequence is the
XX      Human KDR/FLK-1 mutant where Tyr at 1214 is replaced by Phe. Note: The
XX      present sequence is not shown in the specification but was created by the
XX      indexer using the KDR/FLK-1 sequence appearing as AAU7926 and the
XX      information in example 8
XX      Sequence 1356 AA;

Query Match      85.5%; Score 53; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DGKDYIVLPI 11
      |||||
DB      1171 DGKDYIVLPI 1180

RESULT 15
AAU79426
ID      AAU79426 standard; protein; 1356 AA.
XX
XX      AAU79426;
AC
XX
XX      02-JUL-2002 (first entry)
DT
XX
XX      Human Kinase insert domain-containing receptor.
DE
XX
XX      Human; KDR; kinase insert domain-containing; receptor; FLK-1;
KW      fetal liver kinase-1; cytostatic; antidiabetic; antirheumatic;
KW      antiarthritic; signal transduction; phosphorylation; cell proliferation;
KW      angiogenesis; tumour; diabetic omentopathy; chronic rheumatoid arthritis.
XX
XX      Homo sapiens.
OS
XX
XX      WO200229090-A1.
PN
XX
XX      11-APR-2002.
PD
XX
XX      02-OCT-2001; 2001WO-JP008684.
PF
XX
XX      03-OCT-2000; 2000JP-00303694.
PR
XX
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
PA      (SHIB/) SHIBUYA M.
XX
XX      Shibuya M, Takahashi T, Furuya A, Shitara K;
PI      WPI; 2002-352237/38.
XX
XX      Screening substances inhibiting the binding of signal-transducing
PT      molecule to KDR/Flk-1 phosphorylated at tyrosine at 1175-position, as
PT      cell proliferation inhibitors and angiogenesis inhibitors for treatment
PT      of e.g. tumor.
XX
XX      Disclosure; Page 65-71; 81pp; Japanese.
XX
XX      The invention relates to inhibiting the signal transduction of KDR/Flk-1
XX      (kinase insert domain-containing receptor/fetal liver kinase-1) is by
XX      using a substance inhibiting the binding of a signal-transducing molecule
XX      to KDR/Flk-1 phosphorylated at tyrosine at the 1175-position. Also
XX      included are methods of detecting/inhibiting/screening for cell
XX      proliferation, angiogenesis, KDR/Flk-1 signal transduction and KDR/Flk-1
XX      phosphorylation at tyrosine at the 1175-position using the binding
XX      inhibitors, compounds obtained by the screening methods, drugs containing
XX      the inhibitors, a monoclonal antibody or its fragment recognising KDR/Flk-
XX      -1 phosphorylated at tyrosine at the 1175-position, a DNA encoding the
XX      monoclonal antibody or its fragment, a recombinant vector containing the
XX      DNA and a transformant obtained by transferring the recombinant vector
XX      into a host cell. The method is useful for screening substances
XX      inhibiting the binding of a signal-transducing molecule to KDR/Flk-1
XX      phosphorylated at tyrosine at 1175-position, as cell proliferation
XX      inhibitors and angiogenesis inhibitors for treatment of e.g. tumour,
XX      diabetic omentopathy and chronic rheumatoid arthritis. A method for
XX      detecting angiogenesis is also provided. The present sequence is the
XX      Human KDR/FLK-1 protein
XX
XX      Sequence 1356 AA;

Query Match      85.5%; Score 53; DB 5; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 DGKDYIVLPI 11
| | | | | | | |
Db 1171 DGKDYIVLPI 1180

Search completed: December 9, 2005, 10:28:47
Job time : 60.4906 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 9, 2005, 10:20:05 ; Search time 60.8113 Seconds
(without alignments)
127.621 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKDYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	53	85.5	180	Q8MI23_SHEEP	Q8mi23 ovis aries
2	53	85.5	207	Q9N112_SHEEP	Q9n112 ovis aries
3	53	85.5	1356	1 VGRF2_HUMAN	P35968 homo sapien
4	53	85.5	1451	2 Q59EB0_HUMAN	Q8ceb0 homo sapien
5	50	80.6	341	2 Q8CD05_MOUSE	Q8cd05 mus musculus
6	50	80.6	1343	1 VGRF2_RAT	Q08775 rattus norv
7	50	80.6	1343	2 Q5PQU0_RAT	Q5pqu0 rattus norv
8	50	80.6	1345	2 Q8VCD0_MOUSE	Q8vcd0 mus musculus
9	50	80.6	1348	1 VGRF2_COTJA	P52583 coturnix co
10	50	80.6	1348	2 Q677M1_CHICK	Q677m1 gallus gall
11	50	80.6	1367	1 VGRF2_MOUSE	P35918 mus musculus
12	47	75.8	181	2 Q709P9_HUMAN	Q709p9 homo sapien
13	47	75.8	181	2 Q709Q0_HUMAN	Q709q0 homo sapien
14	47	75.8	181	2 Q8WLT2_HUMAN	Q8wlt2 homo sapien
15	47	75.8	181	2 Q4GX19_HUMAN	Q4gx19 homo sapien
16	47	75.8	273	2 Q8SNC8_HUMAN	Q8snc8 homo sapien
17	47	75.8	304	2 Q8SNC1_HUMAN	Q8snc1 homo sapien
18	47	75.8	445	2 Q7V0C6_PROMP	Q7v0c6 prochloroco
19	46	74.2	415	2 Q4HSF2_CAMUP	Q4hsf2 campylobact
20	46	74.2	416	2 Q4HTW6_CAMLA	Q4htw6 campylobact
21	45	72.6	416	1 PUR2_CAMJE	Q9pm47 campylobact
22	45	72.6	416	1 PUR2_CAMJR	Q5htc11 campylobact
23	45	72.6	416	2 Q4HH59_CAMCO	Q4hh59 campylobact
24	44	71.0	178	2 Q9XS54_RABIT	Q9xs54 coryctolagus
25	44	71.0	217	2 Q4UJ21_THEAN	Q4uj21 theileria a
26	44	71.0	359	2 Q5NTF8_9BACT	Q5ntf8 uncultured
27	44	71.0	431	2 Q7MUW7_FORGI	Q7muw7 porphyromon
28	43	69.4	150	2 Q6M9V0_PARUM	Q6m9v0 parachlamyd
29	43	69.4	419	2 Q7M9I6_WOLSL	Q7m9i6 wolinsella s
30	42	67.7	177	2 Q7YXP4_AOTVO	Q7ypx4 aotus vocif
31	42	67.7	177	2 Q7YXP5_AOTVO	Q7ypx5 aotus vocif

32	42	67.7	177	2	Q7YXP6_AOTVO	Q7ypx6 aotus vocif
33	42	67.7	177	2	Q7YYP2_AOTNI	Q7yyp2 aotus nigri
34	42	67.7	177	2	Q7YYP5_AOTNI	Q7yyp5 aotus nigri
35	42	67.7	177	2	Q7YYP7_AOTNA	Q7yyp7 aotus nancy
36	42	67.7	225	2	Q5QGV8_MACNE	Q5qgv8 macaca neme
37	42	67.7	351	2	Q7OPL5_MACMU	Q7opl5 macaca mula
38	42	67.7	351	2	Q7OPL6_MACMU	Q7opl6 macaca mula
39	42	67.7	354	2	Q5QGW4_MACNE	Q5qgw4 macaca neme
40	42	67.7	355	2	Q5DLS0_AOTNA	Q5dls0 aotus nancy
41	42	67.7	357	2	Q5DLR6_AOTNA	Q5dlr6 aotus nancy
42	42	67.7	357	2	Q5DLR9_AOTNA	Q5dlr9 aotus nancy
43	42	67.7	357	2	Q5DLS1_AOTNA	Q5dls1 aotus nancy
44	42	67.7	357	2	Q5DLT2_AOTVO	Q5dlt2 aotus vocif
45	42	67.7	362	2	Q4W7D8_MACFA	Q4w7d8 macaca fasc

ALIGNMENTS

RESULT 1
Q8MI23_SHEEP PRELIMINARY; PRT; 180 AA.
AC Q8MI23;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vascular endothelial growth factor receptor-2 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placental artery endothelium;
RA Chung J.-Y., Tsol S.C.M., Wen Y.-X., Magness R.R., Zheng J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF534634; AAN04105.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8MI23; 1-150.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1
FT NON_TER 180
SQ SEQUENCE 180 AA; 20599 MW; 70B5F444574779A0 CRC64;
Query Match 85.5%; Score 53; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;
QY 2 DGKDYIVLPI 11
Db 153 DGKDYIVLPI 162
RESULT 2
Q9N112_SHEEP PRELIMINARY; PRT; 207 AA.
ID Q9N112;
AC Q9N112;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

```

DE KDR/flk-1 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Scholz T.D., Segar J.L.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233076; AAF60280.1; -, mRNA.
DR HSP; P35968; 1VR2.
DR SMR; Q9N122; 1-157.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR01834; VEGFRCEPTR2.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1
FT NON_TER 207
FT NON_TER 207
SQ SEQUENCE 207 AA; 23691 MW; 51C3950D82F988F6 CRC64;

Query Match 85.5%; Score 53; DB 2; Length 207;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVLPI 11
Db 160 DGKDYIVLPI 169

RESULT 3
VGFR2 HUMAN STANDARD; PRT; 1356 AA.
AC P35968; O60723; Q14178;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Kinase insert domain receptor) (protein-tyrosine kinase
DE receptor Flk-1).
GN Name=KDR; Synonyms=FLK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yin L.Y., Wu Y., Patterson C.;
RL "Full length human KDR/flk-1 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Umbilical vein;
RA Yu Y., Whitney R.G., Sato J.D.;
RT "Coding region for human VEGF receptor KDR (VEGFR-2)";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 3-1356.
RC TISSUE=Umbilical vein;
RX MEDLINE=92019839; PubMed=1656371;
RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,
RA Shows T.B.;

```

"Identification of a new endothelial cell growth factor receptor tyrosine kinase."; Oncogene 6:1677-1683(1991).

[4]

NUCLEOTIDE SEQUENCE OF 1-22. MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111; Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E., Harber E.;

"Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).

[5]

FUNCTION MEDLINE=93038639; PubMed=1417831; Terman B.I., Dougherty-Vermazen M., Carrion M.E., Dimitrov D., Armellino D.C., Gospodarowicz D., Boehlen P.;

"Identification of the KDR tyrosine kinase as a receptor for vascular endothelial cell growth factor."; Biochem. Biophys. Res. Commun. 187:1579-1586(1992).

-1- FUNCTION: Receptor for VEGF or VEGFR. Has a tyrosine-protein kinase activity. The VEGF-kinase ligand/receptor signaling system plays a key role in vascular development and regulation of vascular permeability.

-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.

-1- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like) domains.

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EMBL; AF035121; AAB88005.1; -, mRNA.

EMBL; AF063658; AAC16450.1; -, mRNA.

EMBL; X61656; CAA43837.1; -, mRNA.

EMBL; L04947; AAA59459.1; -, mRNA.

EMBL; X89776; CAA61916.1; -, Genomic_DNA.

PIR; JCI402; JCI402.

PDB; 1VR2; X-ray; A=806-1171.

Ensembl; ENSG00000128052; Homo sapiens.

HGNC; HGNC:6307; KDR.

MIM; 191306; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.

GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_c2.

InterPro; IPR00719; Prot_kinase.

InterPro; IPR001824; RecepttyrkinIII.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR008266; Tyr_pkinase_AS.

InterPro; IPR009134; VEGFR.

InterPro; IPR009136; VEGFR2.

PRINTS; PR01832; VEGFRECEPTOR.

PRINTS; PR01834; VEGFRECEPTR2.

PRODOM; PD000001; Prot_kinase; 2.

SMART; SM00408; Igc2; 2.

SMART; SM00219; Tyrkc; 1.

PROSITE; PS50835; IG_LIKE; 5.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

3D-structure; Angiogenesis; ATP-binding; Developmental protein; Differentiation; Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.

SIGNAL 1 19 Potential.


```

FT CHAIN 20 1356 Vascular endothelial growth factor
FT receptor 2.
FT Extracellular (Potential).
FT Transmem 764
FT TOPO_DOM 755
FT TRANSMEM 789
FT TOPO_DOM 1356
FT DOMAIN 46 110 Cytoplasmic (Potential).
FT DOMAIN 141 207 Ig-like C2-type 1.
FT DOMAIN 224 320 Ig-like C2-type 2.
FT DOMAIN 328 414 Ig-like C2-type 3.
FT DOMAIN 421 548 Ig-like C2-type 4.
FT DOMAIN 551 660 Ig-like C2-type 5.
FT DOMAIN 667 753 Ig-like C2-type 6.
FT DOMAIN 834 1162 Ig-like C2-type 7.
FT NP_BIND 1028 Protein kinase.
FT BINDING 868 ATP (By similarity).
FT MOD_RES 1059 ATP (By similarity).
FT Phosphotyrosine (By autocatalysis) (By
FT similarity).
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 66 66 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 96 96 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 318 318 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 395 395 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 523 523 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 580 580 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 613 613 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 619 619 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 631 631 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 675 675 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 704 704 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 721 721 N-linked (GlcNAc...) (Potential).
FT VARIANT 297 V -> I (in dbSNP:2305948).
FT VARIANT 472 /FTID=VAR_022071.
FT VARIANT 472 Q -> H (in dbSNP:1870377).
FT CONFLICT 2 /FTID=VAR_020353.
FT CONFLICT 772 Q -> E (in Ref. 2).
FT CONFLICT 787 A -> T (in Ref. 3).
FT CONFLICT 835 R -> G (in Ref. 3).
FT CONFLICT 848 K -> N (in Ref. 3).
FT CONFLICT 848 V -> E (in Ref. 3).
FT CONFLICT 1347 S -> T (in Ref. 3).
FT CONFLICT 1356 S -> T (in Ref. 3).
FT SEQUENCE 1356 AA; 151527 MW; 59E7C44B05CFEBB3 CRC64;

Query Match 85.5%; Score 53; DB 1; Length 1356;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
DB 1171 DGKDYIVLPI 1180
|||||

RESULT 4
Q59EB0 HUMAN PRELIMINARY; PRT; 1451 AA.
AC Q59EB0.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Kinase insert domain receptor (A type III receptor tyrosine kinase)
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209901; BAD93138.1; -, mRNA.
KW Kinase; Receptor.
FT NON_TER 1
FT SEQUENCE 1451 AA; 161601 MW; 915FE64B51EFAOCB CRC64;

Query Match 85.5%; Score 53; DB 2; Length 1451;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11
DB 1266 DGKDYIVLPI 1275
|||||

RESULT 5
Q8CD05 MOUSE PRELIMINARY; PRT; 341 AA.
ID Q8CD05.
AC Q8CD05.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 14 days embryo thymus cDNA, RIKEN full-length enriched
DE library, clone:6130401C07 product:kinase insert domain protein
DE receptor, full insert sequence. (Fragment).
DE Name=Kdr;
GN Mus musculus (Mouse).
OS Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

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RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUB=Thymus;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUB=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUB=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031739; BAC27532.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q8CD05; 1-162.
DR MGI; MGI:36683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR GO; GO:0030097; P:hemoiesis; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009136; VEGFR2.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR01634; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Kinase Receptor.
FT NON_TER
SQ SEQUENCE 341 AA; 38302 MW; E2B4DCC4BB481195 CRC64;
Query Match 80.6%; Score 50; DB 2; Length 341;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGKDYVLPI 11
Db 165 DGKDYVLPI 174
RESULT 6
VGFR2_RAT

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ID VGFR2_RAT STANDARD; PRT; 1343 AA.
AC Q08775;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1).
GN Name=Kdr; Synonyms=Flk1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUB=Retina;
RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -1- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U93306; AAB97508.1; -; mRNA.
DR EMBL; U93307; AAB97509.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR RGD; 2965; Kdr.
DR GO; GO:0019838; F:growth factor binding; IMP.
DR GO; GO:0005021; P:vascular endothelial growth factor receptor. ; IMP.
DR GO; GO:0048010; P:vascular endothelial growth factor receptor. ; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinasII.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1343 Vascular endothelial growth factor
FT receptor 2.
FT TOPO_DOM 20 760 Extracellular (Potential).
FT TRANSMEM 761 782 Potential.
FT TOPO_DOM 783 1343 Cytoplasmic (Potential).

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FT	DOMAIN	46	109	Ig-like C2-type 1.			
FT	DOMAIN	141	207	Ig-like C2-type 2.			
FT	DOMAIN	224	320	Ig-like C2-type 3.			
FT	DOMAIN	328	414	Ig-like C2-type 4.			
FT	DOMAIN	421	540	Ig-like C2-type 5.			
FT	DOMAIN	547	654	Ig-like C2-type 6.			
FT	DOMAIN	663	749	Ig-like C2-type 7.			
FT	DOMAIN	830	1158	Protein kinase.			
FT	NP_BIND	836	844	ATP (By similarity).			
FT	ACT_SITE	1024	1024	By similarity.			
FT	BINDING	864	864	Phosphotyrosine (by autocatalysis) (By similarity).			
FT	MOD_RES	1055	1055	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	46	46	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	96	96	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	143	143	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	158	158	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	245	245	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	318	318	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	374	374	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	395	395	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	507	507	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	576	576	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	609	609	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	615	615	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	627	627	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	671	671	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	700	700	N-linked (GlcNAc. .) (Potential).			
FT	CARBOHYD	717	717	N-linked (GlcNAc. .) (Potential).			
SQ	SEQUENCE	1343 AA;	150394 MW; AD/ES09EB62D3FF4 CRC64;				
				Query Match 80.6%; Score 50; DB 1; Length 1343;			
				Best Local Similarity 90.0%; Pred. No. 5.5;			
				Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Oy	2 DGKDYIVLPI 11						
	:						
Dd	1167 DGRDYIVLPM 1176						
<hr/>							
RESULT 7							
QSPOUO_RAT PRELIMINARY; PRT; 1343 AA.							
ID	QSPOUO_RAT	AC QSPOUO;					
DT	01-FEB-2005 (TrEMBLrel. 29, Created)						
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)						
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)						
Kdr protein.							
DE	Name=Kdr;						
GN	Rattus norvegicus (Rat).						
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;						
OC	Muridae; Murinae; Rattus.						
NCBI_TaxID=10116;							
[1]	NUCLEOTIDE SEQUENCE.						
TISSUE=Lung.							
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;						
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,						
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,						
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,						
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,						
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,						
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,						
RA	Brownstein M.J., Uesdin T.B., Toshituki S., Carninci P., Prange C.,						
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,						
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,						
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,						
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,						
RA	Faney J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,						
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,						
RA	Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,						
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,						

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-FVB/N; TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020530; AAH20530.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR Ensembl; ENSMUSG0000062960; Mus musculus.
DR MGI; MGI:96683; Kdr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0045165; P:cell fate commitment; IMP.
DR GO; GO:0016477; P:cell migration; IGI.
DR GO; GO:0045446; P:endothelial cell differentiation; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTOR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1345 AA; 150460 MW; 11859F9A58A33A39 CRC64;

Query Match 80.6%; Score 50; DB 2; Length 1345;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGKQVIVLPI 11
|||||||
Db 1169 DGKQVIVLPM 1178

RESULT 9
VGFR2_COTJA STANDARD; PRT; 1348 AA.
AC P52583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Endothelial kinase receptor EK1) (Quek 1) (Quek1).
GN Name=KDR; Synonyms=EK1, FLK-1;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=97017121; PubMed=8863722; DOI=10.1016/0378-1119(96)00159-X;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Molecular cloning of Quek 1 and 2, two quail vascular endothelial
RT growth factor (VEGF) receptor-like molecules."; Gene 174:3-8(1996).
RL [2]
RN NUCLEOTIDE SEQUENCE OF 910-1348.
RP TISSUE=Spinal cord;
RX MEDLINE=93378866; PubMed=8396413; DOI=10.1016/0925-4773(93)90096-G;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Two molecules related to the VEGF receptor are expressed in early
RT endothelial cells during avian embryonic development."; Mech. Dev. 42:33-48(1993).
RL [3]
RN NUCLEOTIDE SEQUENCE OF 764-880, AND CHARACTERIZATION.
RP TISSUE=Embryo;
RX MEDLINE=95301109; PubMed=7781909; DOI=10.1006/dbio.1995.1180;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1)
RT are expressed during vasculogenesis and vascular differentiation in
RT the quail embryo."; Dev. Biol. 169:699-712(1995).
RL [4]
RN NUCLEOTIDE SEQUENCE OF 1023-1079.
RP PubMed=1281306;
RX Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RT the avian embryo."; Oncogene 7:2479-2487(1992).
CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In all endothelial tissues during onset of
CC vascularization. In later development, present in lung, heart,
CC intestine and skin.
CC -!- DEVELOPMENTAL STAGE: Expressed in whole mesoderm at onset of
CC gastrulation. From day 2, confined to endothelial tissues and
CC expression continues to be widespread throughout vascularization
CC until E9 where it becomes restricted to specific regions such as
CC the spinal chord and heart valves.
CC -!- INDUCTION: In vitro, it is induced by basic fibroblast growth
CC factor (bFGF), uniquely in the first 24 hours of cell culture.
CC -!- SIMILARITY: Belongs to the tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; X83288; CAA58268.1; -; mRNA.
CC EMBL; S65205; AAB28127.1; -; mRNA.
CC EMBL; S78345; AAB34594.1; -; mRNA.
CC PIR; JC4953; S51656.
CC HSSP; P35968; 1VR2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001824; RecepttyrkinsIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR008266; Tyr_pkinase_AS.

```

DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; ig_1.
DR PRINTS; PR01832; VEGPRECEPTOR.
DR PRINTS; PR01834; VEGPRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Angiogenesis; ATP-binding; Developmental protein; Differentiation;
KW Glycoprotein; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 20
FT CHAIN 21 1348
FT TOPO_DOM 21 756
FT TRANSMEM 757 777
FT TOPO_DOM 778 1348
FT DOMAIN 43 106
FT DOMAIN 138 202
FT DOMAIN 220 312
FT DOMAIN 320 405
FT DOMAIN 412 534
FT DOMAIN 540 651
FT DOMAIN 658 744
FT DOMAIN 825 1155
FT NP_BIND 831 839
FT ACT_SITE 1021 1021
FT BINDING 859 859
FT CARBOHYD 43 43
FT CARBOHYD 47 47
FT CARBOHYD 63 63
FT CARBOHYD 93 93
FT CARBOHYD 138 138
FT CARBOHYD 153 153
FT CARBOHYD 201 201
FT CARBOHYD 240 240
FT CARBOHYD 290 290
FT CARBOHYD 310 310
FT CARBOHYD 365 365
FT CARBOHYD 386 386
FT CARBOHYD 513 513
FT CARBOHYD 556 556
FT CARBOHYD 603 603
FT CARBOHYD 613 613
FT CARBOHYD 622 622
FT CARBOHYD 666 666
FT CARBOHYD 688 688
FT CARBOHYD 710 710
FT CONFLICT 865 865
FT SEQUENCE 1348 AA; 150306 MW; A5E419A76FD5FB3 CRC64;

Query Match 80.6%; Score 50; DB 1; Length 1348;
Best Local Similarity 80.0%; Pred. No. 5.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYVLP 11
Db 1164 DGKDYVLP 1173

RESULT 10
Q677M1.CHICK PRELIMINARY; PRT; 1348 AA.
AC Q677M1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

```

```

DE Vascular endothelial growth factor receptor 2.
GN Name=Flk1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Hashimoto T.;
RT "Modulation of retinal neurogenesis by vascular endothelial growth
factor.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY328882; AAR26285.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR InterPro; IPR009136; VEGFR2.
DR Pfam; PF00047; ig_1.
DR PRINTS; PR01832; VEGPRECEPTOR.
DR PRINTS; PR01834; VEGPRECEPTR2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 5.
DR SMART; SM00408; IGC2; 5.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Receptor.
SQ SEQUENCE 1348 AA; 150121 MW; F6EFOF21CA839D6E CRC64;

Query Match 80.6%; Score 50; DB 2; Length 1348;
Best Local Similarity 80.0%; Pred. No. 5.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYVLP 11
Db 1164 DGKDYVLP 1173

RESULT 11
VGFR2_MOUSE
ID VGFR2_MOUSE STANDARD; PRT; 1367 AA.
AC P35918;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1) (Kinase NYK).
GN Name=Kdr; Synonyms=Flk-1, Flk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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Query Match      80.6%; Score 50; DB 1; Length 1367;
Best Local Similarity 90.0%; Pred. No. 5.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 11
   |||||
Db 1169 DGKDYIVLPM 1178

RESULT 12
Q709P9 HUMAN
ID Q709P9 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q709P9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral blood;
RA Darke C., Hammond L., Street J., Downing J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ606948; CAES4963.1; -; Genomic_DNA.
DR HSSP; P30474; IAIN.
DR SMR; Q709P9; 1-181.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_1;
DR Pfam; PF00129; MHC_I_1;
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I_1;
FT NON_TER 181
FT NON_TER 181
SQ SEQUENCE 181 AA; 20972 MW; 80CB6E6E284E65E2 CRC64;

Query Match      75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
   |||||
Db 117 CDGKDYIAL 125

RESULT 13
Q709Q0 HUMAN
ID Q709Q0 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q709Q0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral blood;
RA Darke C., Hammond L., Street J., Downing J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ606947; CAES4962.1; -; Genomic_DNA.
DR HSSP; P30474; IAIN.
DR SMR; Q709Q0; 1-181.

Query Match      75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
   |||||
Db 117 CDGKDYIAL 125

RESULT 14
Q8WLT2 HUMAN
ID Q8WLT2 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q8WLT2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bennett T.T., Cavett J.W., Sidebottom D.A., Bardet W., Pruett B.N.,
RA Orina J., Luis A.D., Hildebrand W.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY045736; AAL10679.1; -; Genomic_DNA.
DR EMBL; AY045735; AAL10679.1; JOINED; Genomic_DNA.
DR HSSP; P30474; IAIN.
DR SMR; Q8WLT2; 1-181.
DR GO; GO:0042612; C:MHC class I protein complex; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019882; P:antigen presentation; IEA.
DR InterPro; IPR001039; MHC_I_alpha_ALA2.
DR Pfam; PF00129; MHC_I_1;
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I_1;
FT NON_TER 181
FT NON_TER 181
SQ SEQUENCE 181 AA; 20972 MW; 80CB6E6E284E65E2 CRC64;

Query Match      75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
   |||||
Db 117 CDGKDYIAL 125

RESULT 15
Q4GX9 HUMAN
ID Q4GX9 HUMAN PRELIMINARY; PRT; 181 AA.
AC Q4GX9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE HLA Class I antigen (Fragment).
GN Name=HLA-B;
OS Homo sapiens (Human).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN {1}

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=41241; TISSUE=Peripheral blood;
RA Hammond L., Street J., Darke C.;
RT "Confirmatory sequence and serology of HLA-B*3541.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AM040977; CAJ13856.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 20972 MW; 80CB6E6E284E65E2 CRC64;

Query Match 75.8%; Score 47; DB 2; Length 181;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CDGKDYIVL 9
Db 117 CDGKDYIAL 125

Search completed: December 9, 2005, 10:33:45
Job time : 62.8113 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:21:00 ; Search time 9.54717 Seconds
(without alignments)
110.858 Million cell updates/sec

Title: US-10-763-276-1
Perfect score: 62
Sequence: 1 CDGKYIVLPI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	85.5	1356	JC1402	protein-tyrosine k
2	50	80.6	1348	S51656	vascular endotheli
3	50	80.6	1367	A41228	protein-tyrosine k
4	45	72.6	416	D81332	phosphoribosylamin
5	41.5	66.9	662	T44219	hypothetical prote
6	41.5	66.9	662	T44034	hypothetical prote
7	40	64.5	108	C72231	ATP synthase Fl, s
8	40	64.5	984	H90029	hypothetical prote
9	39	62.9	598	F83977	hypothetical prote
10	39	62.9	633	T23090	hypothetical prote
11	39	62.9	953	R82068	valyl-tRNA synthet
12	38.5	62.1	788	I159282	diacylglycerol kin
13	38	61.3	84	S51100	hypothetical prote
14	38	61.3	89	T72029	MHC HLA-A3-alpha-2
15	38	61.3	89	I56009	MHC HLA-A2-alpha-2
16	38	61.3	137	T180172	class I histocompa
17	38	61.3	137	T180175	class I histocompa
18	38	61.3	137	T180173	class I histocompa
19	38	61.3	137	T180176	class I histocompa
20	38	61.3	137	T180174	class I histocompa
21	38	61.3	137	T138875	MHC class I antige
22	38	61.3	137	T138860	MHC class I antige
23	38	61.3	137	T138874	MHC class I antige
24	38	61.3	137	T138876	MHC cell surface a
25	38	61.3	181	T179640	MHC cell surface g
26	38	61.3	181	T159188	human leukocyte an
27	38	61.3	182	T49411	HLA-Cw7 - human (f
28	38	61.3	206	T137529	HLA-Cw1 - human (f
29	38	61.3	206	T137528	HLA-Cw1 - human (f

ALIGNMENTS

RESULT 1

JC1402
protein-tyrosine kinase (BC 2.7.1.112) KDR - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 05-Oct-2004
C:Accession: JC1402; I58357
R;Terman, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Gosi;
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
A;Title: Identification of the KDR tyrosine kinase as a receptor for vascular endotheli.
A;Reference number: JC1402; MUID:93038639; PMID:1417831
A;Accession: JC1402
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-48, 'I', 50-616, 'E', 618-700, 'E', 702-748, 'F', 750-1263, 'I', 1265-1290, 'P', 1292
A;Cross-references: UNIPROT:P35968; UNIPARC:UPI000017A3C3; EMBL:X61656; NID:G31717
R;Terman, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.; Shows, T.B.
Oncogene 6, 1677-1683, 1991
A;Title: Identification of a new endothelial cell growth factor receptor tyrosine kinas
A;Reference number: I58357; MUID:92019839; PMID:1656371
A;Accession: I58357
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 3-1356 <TER2>
A;Cross-references: UNIPARC:UPI000016A991; GB:L04947; NID:G186674; PIDN:AAAS9459.1; PID
C;Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.

Query Match

85.5%; Score 53; DB 2; Length 1356;
Best Local Similarity 100.0%; Pred.No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGKDYIVLPI 11

|||||

Db 1171 DGKDYIVLPI 1180

RESULT 2

S51656
vascular endothelial growth factor receptor 1 precursor - Japanese quail
N;Alternate names: quail endothelial kinase 1 (Quek 1); vascular endothelial growth fac
C;Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
C;Accession: JCA4953; AS6598; I51162; S51656
R;Richmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996

A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
A;Reference number: JC4953; MUID:97017121; PMID:8863722
A;Accession: JC4953
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1348 <EIC1>
A;Cross-references: UNIPROT:P52583; UNIPARC:UPI0000138775; EMBL:X83288; NID:G603523; PID:
A;Note: submitted to the EMBL Data Library, December 1994
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Mach. Dev. 42, 33-48, 1993
A;Title: Two molecules related to the VEGF receptor are expressed in early endothelial c
A;Reference number: A56598; MUID:93378866; PMID:8396413
A;Contents: E16 spinal cord
A;Accession: A56598
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 910-1348 <EIC2>
A;Cross-references: UNIPARC:UPI0000171474; GB:S65205; NID:G410680; PIDN:AAB28127.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:137162, NCBI:P:137163)
R;Marcelle, C.; Eichmann, A.
Oncogene 7, 2479-2487, 1992
A;Title: Molecular cloning of a family of protein kinase genes expressed in the avian em
A;Reference number: I50595; MUID:93096482; PMID:1281306
A;Accession: I51162
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1023-1079 <MAR>
A;Cross-references: UNIPARC:UPI00000F94F0; EMBL:X69694; NID:G395226; PIDN:CAA49364.1; PI
A;Note: the species is not identified by the authors; the most probable species is shown
C;Comment: This protein is an endothelial-specific receptor and binds vascular endotheli
C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;120-1348/Product: vascular endothelial growth factor receptor 1 #status predicted <MAT>
F;756-777/Domain: transmembrane #status predicted <TM>
F;823-1160/Domain: protein kinase homology <KIN>
F;831-839/Region: protein kinase ATP-binding motif

Query Match 80.6%; Score 50; DB 2; Length 1348;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DGKDYIVLPI 11
|||:|:|:|:
Db 1164 DGKDYVVLPL 1173

RESULT 3
A41228
protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept
C;Species: Mus musculus (house mouse)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004
C;Accession: A41228; A46065; I58365; I58832; S29991
R;Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A;Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitiv
A;Reference number: A41228; MUID:92020984; PMID:1717995
A;Accession: A41228
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1367 <MAT>
A;Cross-references: UNIPROT:P35918; UNIPARC:UPI0000028D93; GB:X59397; NID:G50976; PIDN:C
R;Millaue, B.; Wizigmann-Voos, S.; Schnurch, H.; Martinez, R.; Mollier, N.P.; Risau, W.;
Cell 72, 835-846, 1993
A;Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a maj
A;Reference number: A46065; MUID:93208880; PMID:7681362
A;Accession: A46065
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-24,'T',26-782,'VL',785-916,'C',918-1367 <MIL>
A;Cross-references: UNIPARC:UPI000003CA97; GB:X70842; NID:G57923; PIDN:CAA50192.1; PID:G
A;Note: submitted to the EMBL Data Library, January 1993
A;Note: sequence extracted from NCBI backbone (NCBI:P:128064)
R;Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemlecki, A.; Wilks, A.F.

Oncogene 8, 11-18, 1993
A;Title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from E10 embryo
A;Reference number: I58365; MUID:93141255; PMID:8423988
A;Accession: I58365
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-678,'D',680-1340,'RSPPV' <OEL>
A;Cross-references: UNIPARC:UPI0000170C47; GB:S53103; NID:G264004; PIDN:AAB25043.1; PID:
C;Genetics:
A;Gene: FLK-1; NYK
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F;830-1165/Domain: protein kinase homology <KIN>
F;838-846/Region: protein kinase ATP-binding motif

Query Match 80.6%; Score 50; DB 2; Length 1367;
Best Local Similarity 90.0%; Pred. No. 1.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DGKDYIVLPI 11
|||:|:|:|:
Db 1169 DGKDYIVLPM 1178

RESULT 4
D81332
phosphoribosylamine-glycine ligase (EC 6.3.4.13) Cj1250 [imported] - Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81332
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: D81332
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <PAR>
A;Cross-references: UNIPROT:Q9PN47; UNIPARC:UPI0000132A1B; GB:AL139077; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: purD; Cj1250
C;Superfamily: phosphoribosylamine-glycine ligase; phosphoribosylamine-glycine ligase ho
C;Keywords: ligase

Query Match 72.6%; Score 45; DB 2; Length 416;
Best Local Similarity 60.0%; Pred. No. 2.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CDGKDYIVLP 10
|||:|:|:|:
Db 197 CDGNDFVLLP 206

RESULT 5
T44219
hypothetical protein U74 [imported] - human herpesvirus 6 (strain Z29)
C;Species: human herpesvirus 6
A;Variety: strain Z29
C;Accession: T44219
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
R;Domínguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A;Reference number: Z22734; MUID:99412318; PMID:10482553
A;Accession: T44219
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-662 <DOM>
A;Cross-references: UNIPROT:P52451; UNIPARC:UPI000012C60D; EMBL:AF157706; PIDN:AAB06357.
A;Experimental source: strain Z29; variant B
C;Genetics:
A;Note: U74

```
Query Match          66.9%; Score 41.5; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 CDGKD-YIVLPI 11
Db 462 CDGKDSHVWVPL 473
||||| :||:

RESULT 6
T44034
hypothetical protein U74 [imported] - human herpesvirus 6 (strain HST)
C:Species: human herpesvirus 6
A:Variety: strain HST
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44034
R:Iseigawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawase, J.; Iseigawa, Y.; 8053-8063, 1999
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: 222732; MUID:99412319; PMID:10482554
A:Accession: T44034
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-662 <ISE>
A:Cross-references: UNIPROT:Q9WT01; UNIPARC:UPI00000FOBBB; EMBL:AB021506; NID:G4995977;
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U74

Query Match          66.9%; Score 41.5; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 CDGKD-YIVLPI 11
Db 462 CDGKDSHVWVPL 473
||||| :||:

RESULT 7
C72231
ATP synthase F1, subunit epsilon - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72231
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72231
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <ARN>
A:Cross-references: UNIPROT:Q9X1US; UNIPARC:UPI0000126520; GB:AE001805; GB:AE000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1609

Query Match          64.5%; Score 40; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDGKDYIVL 9
Db 67 CDGKDVIII 75
||||| :||:

RESULT 8
H90029
hypothetical protein SA2102 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
```

```
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2004
C:Accession: H90029
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90029
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-984 <KUR>
A:Cross-references: UNIPROT:Q99RW4; UNIPARC:UPI00000D7F6F; GB:BA000018; PID:gl3702109;
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2102
C:Superfamily: NAD-dependent formate dehydrogenase, alpha subunit

Query Match          64.5%; Score 40; DB 2; Length 984;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGKDYIVLP 10
Db 10 DGKDYIVLP 18
||||| :||:

RESULT 9
R83977
hypothetical protein BH2622 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: R83977
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: R83977
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-598 <STO>
A:Cross-references: UNIPROT:Q9KM3; UNIPARC:UPI00000C3F65; GB:AP001516; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2622
C:Superfamily: Escherichia coli plasmid ColV-K30 aerobactin biosynthesis protein iuca

Query Match          62.9%; Score 39; DB 2; Length 598;
Best Local Similarity 45.5%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CDGKDYIVLPI 11
Db 230 CQADDYVLLPV 240
||||| :||:

RESULT 10
T23090
hypothetical protein H13N06.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23090
R:Lennard, N.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z19673
A:Accession: T23090
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-633 <WIL>
A:Cross-references: UNIPROT:Q9XTQ6; UNIPARC:UPI000017BA61; EMBL:Z99942; PIDN:CAB17071.1
A:Experimental source: clone H13N06
C:Genetics:
A:Gene: CESP:H13N06.6
```

A;Map position: X
A;Introns: 134/3; 179/3; 206/3; 381/2; 420/3; 541/2

Query Match 62.9%; Score 39; DB 2; Length 633;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CDGKDYIVLP 10
||:|||||
Db 171 CDSRDYAFLP 180

RESULT 11

E82068
valyl-tRNA synthetase VC2503 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82068
F;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82068
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-953 <HEI>
A;Cross-references: UNIPROT:Q9KPF73; UNIPARC:UPI000013670E; GB:AE004320; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2503
A;Map position: 1
C;Superfamily: valine-tRNA ligase

Query Match 62.9%; Score 39; DB 2; Length 953;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
|||||||
Db 212 DGKDYIVV 219

RESULT 12

I59282
diacylglycerol kinase (EC 2.7.1.107) gamma - rat
C;Species: *Rattus sp.* (rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I59282
R;Goto, K.; Funayama, M.; Kondo, H.
Proc. Natl. Acad. Sci. U.S.A. 91, 13042-13046, 1994
A;Title: Cloning and expression of a cytoskeleton-associated diacylglycerol kinase that
F;172-204/Domain: calmodulin repeat homology <EF1>
A;Reference number: 159282; MUID:95108095; PMID:7809169
A;Accession: I59282
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-788 <RES>
A;Cross-references: UNIPARC:UPI000012DD22; GB:D38448; NID:g643598; PIDN:BAA07480.1; PID:
C;Superfamily: human diacylglycerol kinase; calmodulin repeat homology; protein kinase C
C;Keywords: ATP; calcium binding; duplication; EF hand; phosphotransferase; zinc
F;172-204/Domain: calmodulin repeat homology <EF1>
F;217-249/Domain: calmodulin repeat homology <EF2>
F;269-318/Domain: protein kinase C zinc-binding repeat homology <KZI>
F;334-380/Domain: protein kinase C zinc-binding repeat homology <KZ2>

Query Match 62.1%; Score 38.5; DB 1; Length 788;
Best Local Similarity 61.5%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

Qy 1 CDG---KDVIIVLP 10
|||:|||||
Db 380 CDGELKDHILLP 392

RESULT 13

S51100
hypothetical protein 3 - human
C;Species: *Homo sapiens* (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51100
R;Blasczyk, R.; Wehling, J.; Salama, A.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51099
A;Accession: S51100
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <BLA>
A;Cross-references: UNIPROT:P16190; UNIPARC:UPI0000016AA55; EMBL:X83005; NID:g619869; PID:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 61.3%; Score 38; DB 2; Length 84;
Best Local Similarity 87.5%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
|||||||
Db 22 DGKDYIAL 29

RESULT 14

I72029
MHC HLA-A3-alpha-2 protein - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I72029
R;Sire, J.; Chimini, G.; Boretto, J.; Toubert, A.; Kahn-Perles, B.; Layet, C.; Sodoyer, H.
J. Immunol. 140, 2422-2430, 1988
A;Title: Hybrid genes between HLA-A2 and HLA-A3 constructed by in vivo recombination all
A;Reference number: I56009; MUID:88170828; PMID:2450922
A;Accession: I72029
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPROT:Q30177; UNIPARC:UPI0000089D17; GB:M20179; NID:g188495; PIDN:
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:I19310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 61.3%; Score 38; DB 2; Length 89;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DGKDYIVL 9
|||||||
Db 26 DGKDYIAL 33

RESULT 15

I56009
MHC HLA-A2-alpha-2 protein - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56009
R;Sire, J.; Chimini, G.; Boretto, J.; Toubert, A.; Kahn-Perles, B.; Layet, C.; Sodoyer, H.
J. Immunol. 140, 2422-2430, 1988
A;Title: Hybrid genes between HLA-A2 and HLA-A3 constructed by in vivo recombination all
A;Reference number: I56009; MUID:88170828; PMID:2450922
A;Accession: I56009
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPROT:Q30176; UNIPARC:UPI0000089A2B; GB:M20139; NID:g188493; PIDN:

A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 61.3%; Score 38; DB 2; Length 89;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGKDYIVL 9
| | | | |
Db 26 DGKDYIAL 33

Search completed: December 9, 2005, 10:34:37
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